



20010-04USA.ST25

SEQUENCE LISTING

<110> POSCO
POSTECH
An, Gynheung
Ryu, Choong-Hwan
Han, Jong-Jin
Kang, Hong-Gyu
An, Kyungsook

<120> ORGAN PREFERENTIAL GENES IDENTIFIED BY T-DNA INSERTIONAL
MUTAGENESIS OF RICE

<130> 20010-04USA

<150> 60/427,166

<151> 2002-11-15

<160> 83

<170> FastSEQ for windows Version 4.0

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<211> 474

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (394)...(474)

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<211> 194

<212> DNA

<213> Oryza sativa

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<222> (104)...(194)

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<211> 325

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<213> Oryza sativa

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 <211> 650
 <212> DNA
 <213> Oryza sativa

<220>
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 <222> (560)...(650)
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 <213> Oryza sativa

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 <223> segment of the T-DNA insert in line 1B-138-07

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<212> DNA

<213> Oryza sativa

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<210> 7

<211> 246

<212> DNA

<213> Oryza sativa

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 <212> DNA
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 <223> segment of the T-DNA insert in line 1C-017-14

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<210> 9
 <211> 214
 <212> DNA
 <213> Oryza sativa

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 <222> (126)...(214)
 <223> segment of the T-DNA insert in line 1C-038-56

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<210> 10
 <211> 514
 <212> DNA
 <213> Oryza sativa

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 <222> (1)...(113)
 <223> segment of the T-DNA insert in line 1C-041-47

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<210> 11
 <211> 603
 <212> DNA

<213> *Oryza sativa*

<220>

<221> misc_feature

<222> (512)...(603)

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<210> 12

<211> 401

<212> DNA

<213> *Oryza sativa*

<220>

<221> misc_feature

<222> (1)...(96)

<223> segment of the T-DNA insert in line 1C-109-35

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<210> 13

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<212> DNA

<213> *Oryza sativa*

<220>

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<222> (528)...(628)

<223> segment of the T-DNA insert in line 1C-109-51

<400> 13

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gtgttgcgag tagcactgtg tgctggggaa gatcattgcc tgcccatctg gtggttggtga 240
tggaaccaca gtattatgat ggccgggaga atgctcatalc tgattatcca atcactgatc 300
tactccaaat gatgggtcat gctagcaggc ctcttcaaga taactcaggg aaatgtgtta 360
tattgtgtca tgcgcctcgc aaggaatact acaagaagtt cttttttgag gccttccctg 420
ttgagagcca tcttcaccac ttcttgcatt atcatatgaa cgctgagggt gtggttggtg 480
tcatagaaaa caagcaagat gctgtggatt accttacttg gaccttcatt tcaaacacgg 540
atccgaggta ccaggtaacca ggtgagttcc attcttacta ccacgggtgct attttttttg 600
ctatgtggct aattacatga ctaacttg                                     628
```

<210> 14

<211> 377
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (1)...(61)
 <223> segment of the T-DNA insert in line 1C-056-07

<400> 14
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 tttcttcagc attaacacag tgtactacat ggcacccttt gccaccatga tactggctct 120
 accagcagtg ttacttgaag gaggcggtgt ggttacctgg ttctacacac atgactccat 180
 tgcttctgca ctagtatatca tcataggctc tggagtgctt gcattttgcc taaacttctc 240
 cattttctac gtgatccatt caaccactgc agtgaccttc aatggttgctg gcaacctgaa 300
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 gaactgatca ttgcgct 377

<210> 15
 <211> 422
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (351)...(422)
 <223> segment of the T-DNA insert in line 1C-100-32

<400> 15
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 aactcaatat gctaccact aatatctagg agttaccatt gtactaaaaa tgtataaaac 120
 atggtttgata ggagttcaga aagtgcattt atctgggtac atccgatcac tggtagaata 180
 tgttaccact tgaaccaaac tttatgtaat ttataatggg atatttgcaa ctacggaatc 240
 ttttactgct catgcaggat cacaaaggaa tttcaaagtc tgcaccagct gattgtccat 300
 tgatcccact attggtgcca aaagtagatc aatcagaagg tacagtggat accagggtgag 360
 ttccattctt actaccacgg tgctattttt tttgctatgt ggctaattac atgactaact 420
 tg 422

<210> 16
 <211> 335
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (259)...(335)
 <223> segment of the T-DNA insert in line 1C-142-27

<400> 16
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 ttggttcgat agcaaccgct gcagttgcaa atttgcaata ttgttttagcg agtagcagcc 120
 tgcactgtcg ttgattgagg attcgttgct tgttttgcct accgtcatgg gcctttttca 180
 ggtcaccgac cgcacgcagg ataagagcca agattctgta cgcgacgtcg aagcaagggc 240
 tgaggcgggt gcttgacgga ggtaccaggt gagttccatt ctactacca cggtgctatt 300
 ttttttgcta tgtggccta tacatgacta acttg 335

<210> 17
 <211> 425
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature

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<222> (332)...(425)

<223> segment of the T-DNA insert in line 1C-140-04

<400> 17

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gctttccagg tatatatata taaaatccat cgatcatgca tgtcagaagc tcatcatgct 60
cagatgctca tcctgctcac gctcaatgct catgctctgc tgaaatttgg cggaatttgt 120
tgcacgcatg ttgtgtttcc gtattgcatc atgtttgtat atgccaagat atgtgcttac 180
taccgtgtga gcaatgctgt tcaagaactg aatttgtttt tgcaaatgtg tcacacctgg 240
agtaggtgga aggggcagct gcagaggatg ggaggaagcc cagcatttgg gacaccttca 300
tccatcaagg tccaaaaaaa tggagtagat gacacggatc cgaggtacca ggtaccaggt 360
gagttccatt cttactacca cgggtgctatt ttttttgcta tgtggctaata tacatgacta 420
acttg
```

<210> 18

<211> 1149

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1B-115-22 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (394)...(395)

<223> location in genomic DNA where T-DNA was inserted
to create line 1B-115-22

<400> 18

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aagcttaata tattaggagt agtaagctag cgtgtgagga agattcataa ccatatatca 60
tccttaattag cctttgtgat ttagcttaat cacatggcta aggcacaacc acccatccac 120
ttaactcttc attactacgc tagctacacg aggagagtag ctagctagta caggccccgg 180
caagcataaa tagcagcgct ccctgcttcc tttcttcacg gtcctcagct catcatctgc 240
atgcagttca ctgcacacca cacagcttag cttgctcagc ttcactgac ttcttagctg 300
cagctacttc actttgcata gtttgatcga actaaataac tcaccaagtt agctgtaatg 360
gccaaagctga tcctcgccac cttcgccgct gtgttcatgg cgctcgccgc cacctccctc 420
gccggcgacc cggacatgct ccaggacgct tgcgtcgccg actacaagtc cctcaaaggc 480
cgtaagtgtt ggaccattat tgttcacgca ttcataaaat atgaattgac ctattttttt 540
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agggcggttc aggtcgacgg cggcatggtc gagttcatca agtccaagtt cgtcccgcgc 1140
aaatactag
```

<210> 19

<211> 2971

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1B-164-43 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (577)...(578)

<223> location in genomic DNA where T-DNA was inserted

to create line 1B-164-43

<400> 19

```

caaaaaggcg cctctaagaa ttcttcccaa acttttttgggt gttgtcaagc cgtgcgtttc 60
ggggtacatc aacggcgggc atgagctccc ggatggcggg atcggcgatc ctccgtcacg 120
tcggcgggcg ccgcctcttc accgcgtcgg cgacctctcc ggcggcggcg gcggcgggcg 180
cggcgaggcc gttccttgca ggcggagaag ccgtcccccg ggtgtggggg ttgcggctga 240
tgtccacgtc gtccgtggcg tcgacggagg cggcgggcaa ggcggaggcc aagaaggcgg 300
acgcggagaa ggagggtggg gtcaacagct actggggcat cgagcagtcg aagaagctgg 360
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tggtttgatt ttctccgcag ccatgggaga cctacaccgc ggacacttcg atcgatctga 600
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```

<210> 20

<211> 4566

<212> DNA

<213> *Oryza sativa*

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1B-192-40 - genomic DNA without T-DNA insert

<221> misc_feature
 <222> (2273)...(2274)
 <223> location in genomic DNA where T-DNA was inserted
 to create line 1B-192-40

```

<400> 20
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caaactagtc atgtttcaaca ggaatgcatt gactattcga ccaagaatat ggcaccatcc 180
aacaatcaac atgggtaaaa gatgtataaa cgcctattaa tataaatgtc ctagtccact 240
ataagaatca aaagcatcta aaaactgaaa ccatattgtc caaaatacac accagcaaag 300
atgggtatgtg cagctataca cattgcagtc gtagcaatgc tcgtctccct tacagcatta 360
gcaatagctg acgaatccga caataaccaa cggaagctc tgctctgcat caaatcacac 420
ctctcaagcc cagagggagg cgccctcacc acatggaaca atacctcgct cgacatgtgc 480
acctggcgcg gcggtgacatg ctccagcgag ctcccaaagc ctggtttggt cgtggccttg 540
gacatggagg cacagggcct cagcggagaa atcccaccct gcatctccaa cctctcgctc 600
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gttgccgggc tccgatacct caacctcagc ttcaacgcga tcggcgggtg gatcccaaaa 720
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```

<210> 21

<211> 1914

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1B-207-27 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (906)...(907)

<223> location in genomic DNA where T-DNA was inserted
to create line 1B-207-27

<400> 21

```

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<210> 22

<211> 6631

<212> DNA

<213> Oryza sativa

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<221> misc_feature

<222> (0)...(0)

<223> line 1B-138-07 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (1310)...(1311)

<223> location in genomic DNA where T-DNA was inserted
to create line 1B-138-07

<400> 22

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<211> 3937
<212> DNA
<213> Oryza sativa

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<221> misc_feature
<222> (0)...(0)
<223> line 1D-059-12 - genomic DNA without T-DNA insert

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<221> misc_feature
<222> (530)...(531)
<223> location in genomic DNA where T-DNA was inserted
to create line 1D-059-12

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<210> 24
<211> 6809
<212> DNA
<213> Oryza sativa
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<220>
<221> misc_feature
<222> (0)...(0)
<223> line 1C-087-40 - genomic DNA without T-DNA insert
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<221> misc_feature
<222> (2666)...(2667)
<223> location in genomic DNA where T-DNA was inserted
to create line 1C-087-40
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<210> 27
<211> 4284
<212> DNA
<213> Oryza sativa

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<220>
<221> misc_feature

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<222> (0)...(0)
 <223> line 1C-041-47 - genomic DNA without T-DNA insert

<221> misc_feature
 <222> (2471)...(2472)
 <223> location in genomic DNA where T-DNA was inserted
 to create line 1C-041-47

```

<400> 27
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```

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```

<210> 28

<211> 3234

<212> DNA

<213> *Oryza sativa*

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-064-20 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (2690)...(2691)

<223> location in genomic DNA where T-DNA was inserted
to create line 1C-064-20

<400> 28

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20010-04USA.ST25

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```

<210> 29

<211> 3677

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-109-35 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (2301)...(2302)

<223> location in genomic DNA where T-DNA was inserted
to create line 1C-109-35

<400> 29

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ggttaatcga tcgccacctg gaccatgcat cctctctata taagctgccc tctaactagc 240
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<210> 30

<211> 8093

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-109-51 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (6570)...(6571)

<223> location in genomic DNA where T-DNA was inserted
to create line 1C-109-51

<400> 30

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tccaaccccc tcttctcccc cttctccggc gcggcgccgg cggcgccatc accggaggcg 180
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20010-04USA.ST25

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<223> line 1C-056-07 - genomic DNA without T-DNA insert

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<223> line 1C-100-32 - genomic DNA without T-DNA insert

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      to create line 1C-100-32

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<211> 2417

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-142-27 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (2020)...(2021)

<223> location in genomic DNA where T-DNA was inserted
to create line 1C-142-27

<400> 33

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<210> 34

<211> 4941

<212> DNA

<213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> line 1C-140-04 - genomic DNA without T-DNA insert

<221> misc_feature
 <222> (773)...(774)
 <223> location in genomic DNA where T-DNA was inserted
 to create line 1C-140-04

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 <211> 672
 <212> DNA
 <213> Oryza sativa

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 <221> misc_feature
 <222> (0)...(0)
 <223> line 18-115-22 coding sequence

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acccgcaccg tctgcaaggg ggaggtgttc gtcttcccgc gggggctcgt ccacttccag 480
aagaacaacg gcaacacgcc ggcgttcgcc atcgccgcct tgaacagcca gctccccggg 540
acgcagtcca tcgccgccgc gctcttcggc gccgcgccgc cgctgccgtc ggacacgctg 600
gccagggcgt tccaggtcga cggcggcatg gtcgagttca tcaagtccaa gttcgtcccc 660
cccaaatact ag
672

```

<210> 36
 <211> 999
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature

<222> (0)...(0)

<223> line 1B-164-43 coding sequence

<400> 36

```

atgagctccc ggatggccgg atcggcgatc ctccgtcacg tcggcggcgt ccgcctcttc 60
accgcgtcgg cgacctctcc ggcggcggcg gcggcggcgg cggcgaggcc gttccttgca 120
ggcgggagaag ccgtcccccg ggtgtggggg ttgcggctga tgtccacgtc gtccgtggcg 180
tcgacggagg cggcggccaa ggcggaggcc aagaaggcgg acgcggagaa ggagggtggtg 240
gtcaacagct actggggcat cgagcagtcg aagaagctgg tgcgggagga cggcacggag 300
tggaagtggg cttgtcttag gccatgggag acctacaccg cggacacttc gatcgatctg 360
acgaagcacc acgtgcccaa gacgtgctc gacaagatcg cctactggac cgtcaagtcg 420
ctgcgcttcc ccactgatat cttcttccag aggagggtatg gctgcccgcg gatgatgctg 480
gagacgggtg cggcgggtgcc ggggatgggt ggcggtatgc tgctccacct ccggtccctc 540
cggcgcttcg agcagagcgg cggctggatc cgcacgctgc tggaagaggc cgagaacgag 600
cgcatgcacc tgatgacctt catggagggt gcgaacccaa agtggtagca gcgcgcccc 660
gtcatcaccg tccagggcgt cttcttcaac gcctacttcc tgggttacct cctctcccc 720
aagttcgcgc accgcgtcgt cggctacctc gaggaggagg ccatccactc gtacaccgag 780
ttcctcaagg acctcgaggc cggcaagatc gacaacgtcc ctgccccggc catcgccatc 840
gactactggc gcctccccgc caacgccacg ctcaaggacg tcgtcaccgt cgtgcgcgcc 900
gacgaggctc accaccgcga cgtcaatcac ttcgcatcgg acatccatta ccagggcag 960
gagctgaagc agacccctgc gccgatcgga tatcactga 999

```

<210> 37

<211> 3216

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1B-192-40 coding sequence

<400> 37

```

atggtatgtg cagctataca cattgcagtc gtagcaatgc tcgtctccct tacagcatta 60
gcaatagctg acgaatccga caataaccaa cgggaagctc tgctctgcat caaatcacac 120
ctctcaagcc cagagggagg cgccctcacc acatggaaca atacctcgct cgacatgtgc 180
acctggcgcg gcgtgacatg ctccagcgag ctcccaaagc ctcgtttggg cgtggccttg 240
gacatggagg cacagggcct cagcggagaa atccccacct gcatctccaa cctctcgctc 300
ctcacgagaa tccacctccc caacaatggc ctctccggtg gcctcgcatc cgcagccgat 360
gttgccgggg tccgatacct caacctcagc ttcaacgcga tcggcgggtg gatcccaaaa 420
cgcttgggta cgcttcgcaa ctttctgtcc ctggacttaa caaacaacaa cattcatggc 480
gagatccccg cgttgcttgg gagctcatct gccttggaat ccgtcgggtc cgccgacaa 540
tacgtgaccg gaggaatccc attgttcttg gctaattgct cctcgctccg ctatctttcc 600
ttgaagaaca atagcctcta tgggagcatc cctgcagcac ttttcaacag ctcaaccatc 660
agggaaatat accttgagaa aaacaatctt tctggtgcaa ttccaccgtt aacaatattc 720
ccttcccaga tcaccaacct tgatcttaca acgaatagcc tgacaggagg cataccacca 780
tctctagggg atctctcatc gcttacagca ctcttagctg cagaaaacca gttgcaggga 840
agtataccgg atttttagtaa actatcggcg ctacggtatc ttgacctctc ttacaacaat 900
ctttctggaa ctgtaaatcc ctccgtttac aacatgtcgt caatcacatt tctcggtttg 960
gccaacaaca atcttgaggg gataatgcct cctggtatag gaaacactct tcctaaccatc 1020
caagtcttga ttatgtctga caatcatttt catggagaaa tccctaaatc tctagcaaat 1080
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ataccacaat ccattggtaa cttgaatcga ttgactgaac tctatttagc agaaaatcaa 1560
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agctggctac tcgatttatc acacaaccaa ttcataaact ccataccact agaacttgg 1740
agcttgataa atcttgcttc tttgaacatt tcccacaaca aatcacaggc caggatccca 1800

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tctacacttg	gttcttgcgt	ccggttggaa	tgcgttcgtg	taggaggcaa	cttcctagag	1860
ggaagtattc	cacaatcatt	agcaaacttc	aggggcacca	aagtgtctga	tttctcccag	1920
aacaatttat	ctggtgcaat	accggatttc	tttgggactt	tcacctcatt	acaatatcta	1980
aatatgtcat	acaacaactt	tgaggggcca	attccagtag	atggaatctt	tgcgacaga	2040
aataagggtg	ttgtccaagg	aaatccacac	ctttgcacca	atgttccaat	ggatgagttg	2100
actgtctgct	ctgcttcagc	atccaaaaga	aagaataagc	tcattattcc	aatgttggca	2160
gctttttcat	ctataatctt	actttcttca	atcctcggat	tatatttctt	gatcgtcaat	2220
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aaaacgttaa	catatagtga	tgtaagcaaa	gcaacaaata	atttttcagc	agccaacata	2340
gttggctctg	ggcatttttg	gacagtctat	agagggtatac	tgcatacaga	agacactatg	2400
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gcatgcgtct	gcgacttttg	tctggcaagg	tcaattcgtg	tttattcatc	tggaactcaa	2820
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tatgtcaatg	catcactttc	acaaatcaaa	gacatacttg	accccaggct	tattccagaa	3060
atgacagagc	aaccttctaa	tcataccctg	caattgcatg	aacacaagaa	gacaccatct	3120
cgatgcaaac	tgggaggggt	ggagggtatt	ctcacatgta	cgataagaga	aattgcatca	3180
aaattaggag	ggcttagatt	atctatgcta	acgtga			3216

<210> 38

<211> 1914

<212> DNA

<213> *Oryza sativa*

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1B-207-27 coding sequence

<400> 38

atgcaagatc	atatacttac	agcttttctg	gttgtttctc	tcctctttgc	atgcattcct	60
cctgccaaaga	gtgctgatct	gaactccgac	aagcaggctc	ttcttgcatt	tgctgcctca	120
ctgccacatg	gcaggaagct	caactggagc	tctgcagccc	cagtctgcac	ttcatgggtt	180
gggggtgactt	gcacaccaga	caatagccgc	gtgcaaacac	tacgcctacc	agcagtaggg	240
ctctttggcc	cgctaccctc	agacacgctt	ggcaagcttg	atgccctgga	ggtattgagc	300
cttaggtcca	atcgcatcac	tgttgatctc	cctctgaag	taggatccat	tccttctctc	360
catttccctat	atcttcagca	taataacccta	tccgggatca	taccgacttc	ccttacttcc	420
actttaacat	ttctagatct	gtcatacaac	actttttagt	gagaaatccc	attgagagtg	480
caaaatctca	ctcaacttac	tgcattgctt	ctccagaata	actctctttc	tggaacctac	540
cctgacctcc	aactcccaaa	attgaggcat	ttgaatttga	gcaacaataa	cctcagtggt	600
ccaataccac	cttccttgca	aagattccca	gccaatccct	tcttggggaa	tgcttttcta	660
tgtgggtttc	ctttacaacc	ttgccctggg	actgcacctt	caccttctcc	ttctccaaca	720
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attgcacttg	ctgccgcagg	aggggtattg	ttgctaactc	tgattgtttt	actcttgata	840
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actgttgctg	gtggaagggg	agaaaatcct	aaggaggagt	acagcagtgg	tggtcaggaa	960
gctgagagga	ataaaattggt	tttctttgag	ggctgttcat	ataattttga	cctagaggat	1020
ttgctgagag	cttcagctga	agtccttgga	aaaggaggtt	acggaaactac	ttataaagct	1080
gttcttgagg	atggcaccac	agttgtgggt	aagagattga	aggaggtggt	cgtaggggaa	1140
aaggattttg	aacagcagat	ggagatagtt	ggcagggttg	gccagcacca	gaatgttgct	1200
ccattgctgt	cctactatta	ctccaaggat	gagaagctac	tggtgtatga	ctatatccca	1260
tctggtagcc	ttgctgttgt	tttgcattgg	aataaagcta	ctggaaaagc	tccattggat	1320
tgggagacga	gggtaaagat	atctcttggt	gtggctcgtg	gaattgtcta	tcttcagtct	1380
gagggagggc	ggaagttcat	ccatggcaac	ctcaagctcat	caaacatcct	tctgtcacag	1440
aacctcgacg	gctgtgtctc	tgagtttggg	ctggcacagc	ttatgaccat	tccaccagct	1500
ccagcacgcc	ttgtcggata	tcgtgcacca	gaagtcctcg	agactaaaaa	gccaaaccag	1560
aagtctgatg	tctacagctt	cgggtgtgtg	gtcctcgaaa	tgctgacagg	aaaagcgcct	1620

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ctgagatctc ctggacgaga ggactccatt gagcacttgc caagggtgggt gcagtcctgtg 1680
gtccgggaag aatggaccgc ggagggtttt gacgtcgact tgtaaaggca tcccaacatt 1740
gaggatgaga tggttcagat gctccagggt gcaatggcat gtgttgccgc cccccctgat 1800
caacggccaa aaatggacga ggtgatcagg aggatcggtt agatccggaa ttcctactcc 1860
gggtcaagaa caccaccgga ggagaagcag aaggatgaat ctgcagcgcc atga 1914

```

<210> 39

<211> 1571

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1B-138-07 coding sequence

<400> 39

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atggccgcgc cgctctccac cgccgcccgc gcctcgtggc tctccgacag cgctcgtct 60
ccgcctaggg tgcgcctcct catcggcggg gagttcgtcg agtcgcgggc cgacgagcac 120
gtcgacgtca ccaatccggc gacgcaggag gtggtgtcgc ggatcccgt caccaccgcc 180
gacgagttca gggccgcccgt ggacgcccgc aggaccgcct tccccgggtg gcggaacacg 240
ccggtgacca cgcggcagcg catcatgtct aagtaccagg agtcatccg ggccaacatg 300
gataaactgg cagagaacat tacaaccgaa caggggaaga cactgaagga tgcttggggc 360
gatgtattcc gtgggctagg tgggtggaaca tgcttgtgga atggggacac tgcagatggg 420
tgaatatgta tcaaatgttt ctaacgggat tgacaccttt agcattaggg agccacttgg 480
tgtatgtgct ggaatatgtc cattcaattt tccagctatg atccccctat ggatgttccc 540
aatagcggtc acttgtggca atacttttgt tctaaagcca tcagaaaaag atccaggggc 600
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gaagcgtggt cagtctaata tgggtgcaaa gaatcatgca attatccttc ctgatgctga 840
ccgagatgcc acactgaatg cccttattgc tgctggtttt ggtgctgctg ggcaaagggtg 900
tatggcattg agcactgctg tttttgttgg aggttcagag ccatggataa gacctggcat 960
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tacaaagtgg tgctgataat ggtgctcgtg tgctgcttga tggagagat attgtggttc 1140
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tagatgatgc tatccaaatt gtgaacagaa acaaatatgg caatggagca tccatattta 1320
caacatctgg tgtgtctgca aggaaatttc aaacagacat tgaagctggc cagggtgggca 1380
tcaacgtgcc gattccagta cccctgccgt tcttctcctt caccggcagc aaagcctcct 1440
ttgcaggaga cttgaatttc tacggcaagg cgggcgtgca gttcttcacc cagatcaaga 1500
cggtcacgca cagtggaag gagtgcggcg ctcagcgcggt ctccctctcc atgcccacct 1560
cgcagaagtg a

```

<210> 40

<211> 1323

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1D-059-12 coding sequence

<400> 40

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atggccgccc cgcgccaccgc cgccgtcccc ctgcacgagg ccaaagccaa ggaggttctc 60
cgccagggtg agttctactt cagcgacagc aacctcccc gcgacaactt cctgcggaag 120
acagtcgagg agagcgagga tggcgtgagc ttggcactca tctgtctcct ctgcggtatg 180
aagaagcacc taggcctgga cgcgacgtg aagcaggaga ccatgccgga ggagacgggtg 240
ctgcgcgttg ctgaggtgct gcggcggttc tcggccctcc gtgtcaccga ggataagaaa 300
gttggttagat caattgagtt gtcgaaactg gatgagatca tggagcaagt ggactctagg 360
acaattgctg catcaccatt tccttacaat gtaaagctgg aagatgttca gtctttcttt 420

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```

gctcagtatg gcaagggtgaa cagtgtgagg ctacctcgac atattgccga caaacgacac 480
ttctgtggca ctgcttttagt cgaattttca gaagaagagg aagcaaagtc tgtattaaag 540
aatactcttg tttttgcagg agcagatctg gaaataaaac caaaagaatt cgatactgaa 600
agagagggcta agaaagaagc ttatgagaag tcacaacctt ctaagaatgg tcatgatgag 660
tatccaaaag gtctaattgt ggctttcaag ctgaagataa ttcaaattga tgggtggcatg 720
gcagaaaatg gtgggggacaa agaggggtgaa actgatgatg ccaataaatc aagaacaggg 780
catgacgaga aaatccctga gaacagtgat atcaaggaag acttgtcaga tgatgtttgag 840
aagtcaaaaag aggcagctgc tcaatctgtt aagaaaggag aaagtccttc agaaaatgcg 900
gatgatccaa tttcaaggga agatttttaa gaagaatttg gcaaattcgg cacagtgcgg 960
tatgtggact tcagcatagg ggaggattca ggatacattc ggttcgagga ttctaaggca 1020
gctgaaaagg cccgtgcact tgcggctatt tcagatgaag gtggtttgat tatgaagggc 1080
catcttggtt ctttggaacc tgtgtctcaa gctgagaagg attattggag tgcgataaag 1140
ggcgggtcaag gaaaatatag agacaataga agtaacaggg gagccgatcc tcttaaata 1200
cataatgcac ctagaatgaa tcttaggagt gggctgaaac ttaaaataga agttgaagcc 1260
ttatggcaca caagaatgcc aacacatata tttggagtta tattatcatg gaactggcag 1320
taa 1323

```

<210> 41

<211> 2568

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-087-40 coding sequence

<400> 41

```

atggccacac gttattggat cgtgtctctt cccgtgcaga ctcttggtct caccgccaat 60
tctctctggg cgcgcctcca ggactccatc tcgcgccact ccttcgacac gccgctctac 120
cggttcaacg tccccgatct ccgcgtcggc acgctcgact ccctcctcgc cctcagcgac 180
gatctcgta agtccaacgt cttcatcgag ggggtctcgc acaagatccg gaggcagatc 240
gaggagctag agcgcgccgg ggggtgtcga agtggggctc tcaccgttga cggcgtcccc 300
gtcgacacct acctcacctt tgtgtgggat gagggcaaat acccaacgat gtcaccgctc 360
aaggagattg tcggcgagcat ccaatcacag gtctccaaga ttgaagatga catgaagggt 420
cgaggagcgg aatacaataa tgtaaggagc cagcttagtg cgatcaacag aaagcaaact 480
ggattagcag ttcgtgatct ttccaatctg gtaaaaccag aggatattgg caccatcagaa 540
catctagtga cactccttgc agttgttctt aagtactctc aaaaggattg gttgtcaagc 600
tatgagtccc ttgacacatt tgtggtaccg agatcgtcta aaaaacttta tgaggacaat 660
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gcacgtgaaa aagggtttcca ggttcgcgat tttgagtata gttctgaagc acaggaaagt 780
aggaaggaa agctggaaaa gctaattgaa gaccaggaag caatgagggc atcacttctg 840
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cagcagcggg ggtgtgggt gaaggaccgg tcgcgcgcgt ggtgggagct gtgcagcagc 1560
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gtctgcgcc ccatccgcaa cctcctcatg ccgcgttcc tccactggcc cgaccacccc 1860
acctccaccg cctacaagac gcgcttcgag gccacctcgg gtgtctcggg ggtgggtggc 1920
gccatgtaca ccacgcacat ccccatcatc gcccccaagg tctccgtcgc cgcttacttg 1980
aaccgccgcc acacggagcg caaccacaag acctcctact ccatcaccct ccagggcgctc 2040
gtcggccccg acggcacctt caccgacgtc tgcatcgggt ggccgggggtc catgagcgac 2100

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cagcgcaacc tgacgtggac gcagcacgcc ttcaacgaga aggtgggcga ggtccggcgc 2280
gtggccacgg aggcgttcgt ccgcctcaag gggcggtggg cgtgcctgca gaagcgacg 2340
gaggtgaagc tgcaggacct ccccgcggtg ctgcgcgcct gctgcgtcct ccacaacatc 2400
tgcgagacca ggggggagga catggacccc gacctccgct gcgacctccc ccccgacgag 2460
gaggaggacg acaccgtgct tgtgcagtcg gagtccgcca acaaggtagg ggacgacatc 2520
gcgcacaacc tcctccaccg cggattggcc ggcaccgcct tcttctga 2568

```

<210> 42

<211> 1413

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-017-14 coding sequence

<400> 42

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atggacgccc tcctcgtgga gaaggctcctc ctgggcctgt tcgtggcggc ggtgctggcc 60
ctagtgggtg ccaagctcac cgggaagagg ctccgcctcc cgcccgcccc cgccggcgcg 120
cccacgtcgc gcaactggct ccaggtcggc gacgacctca accaccgcaa cctgatggcg 180
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cgcacccgca acgtggtggt cgacatcttc accgggaagg ggcaggacat ggtgttcacc 360
gtgtacggcg accactggcg caagatgcgg cggatcatga cggtgccctt cttcaccaac 420
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ccgctcttca acaagctcaa ggccttcaac gcggagcgca gccgcctctc gcagagcttc 660
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ttcgacctgc tgccgcggcc cgggatggac aag 1413

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<210> 43

<211> 1227

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-038-56 coding sequence

<400> 43

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gccgctgtcg ccgtcgccga cccctccccg cggtcggagg tcgtcgacgg cgagagcccg 120
ccgcagccgg gcggcgaggc ggcgagccat cagcagcagc agaaggagat gaagctgaag 180
aagccggaca agatcctgcc atgcccgcgg tgcagcagca tggacaccaa gttctgctac 240
ttcaacaact acaacgtcaa ccagcctcgc cacttctgca agcactgcca gcgctactgg 300
accgccggcg gcgccatgcg caacgtcccc gtcggcgccg gccgccgcaa gaacaagaac 360
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```

ccccgaggcg cccacgacgc caccaacgcc accgtgctca gcttcggcgg cggcggaggc 480
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gaggggctcg tcgcccacgc ccggaacgcc gacgccgcgg ccgctgacag cgagggtgctg 600
agcaacaggg acgacgagca gatcggcaac actgtagcaa aacctgcaaa cgggttgacg 660
cagcatcctc ctctctctca tcatcatcat cattcagcca tgaacggtgg cggcatctgg 720
ccctactaca cctcggggat cgcgatcccg atatacccg cggcgccggc gtactggggc 780
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accagcgtgc acaagctcgc caccacgggtg ttcgagccaa agagggacgg caagacggcg 1140
aaacatccgg cgatcacgag cttgccgctc ttgcacacca accccgctcg gcttaccgca 1200
tccgcgacct tccaggaggg atcttga

```

<210> 44
 <211> 861
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> line 1C-041-47 coding sequence

```

<400> 44
atgggcatca aggggtttgac gaagcttttg gcggacaatg cgccaaggc gatgaaggag 60
cagaagttcg agagctactt cggccggcgc attgccgtcg acgccagcat gagcatctac 120
cagttcctct catttgcata ctggaagagg gaggatgcca ccaaagaact aacagaggca 180
gtagaggaag gagataaaga cgcaattgaa aaattcagca agagaactgt gaagggtcacg 240
aagcagcaca atgaagaatg taaacgacta ttaagactta tgggggttcc tgttgtagag 300
gtttatgcag ttgcatcaga agatatggac tctcttactt ttggagctcc acggtttctt 360
cgctcattga tggatccaag ttccaagaaa attccagtta tggaaattga agtcgcgaaa 420
gttttgagg agcttgaact cactatggac caattcattg acttgatgat cctatctgga 480
tgtgactatt gtgatagcat taaaattgga ggtcaaacag ctctgaaact tattcgtaa 540
catgggtcca tagaaagcat tctggaaaac ataaataaag actatcagat tcctgaggac 600
tggccttatc aagaagctcg acgcttggtt aaggaaacca atgttacatt ggatattcct 660
gagctgaaat ggaatgctcc cgatgaggaa gccatagaga agattaaatt tgccaagaac 720
aaatcttccc aaggactcga atccttcttc aagccagttg ttagcacatc agtcctctg 780
aaaagaaagg acaattcaga aaaaccaacc aaagcagtcg ctaacaagaa aacaaaggga 840
gccggcggaa agaagaaata a

```

<210> 45
 <211> 1653
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> line 1C-064-20 coding sequence

```

<400> 45
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atcgacctcg gaaacgacct ctctgtcggt gcggtgtggc ggcacgaccg cggcgaggtc 120
atcgccaacg accagcgcaa ccgcctcacg ccctcctgcg tcgccttcac cgccgacgac 180
gacgacagct tcgtcggcga cgccgccttc aaccagtcgg cactcaaccc aaccaatacc 240
atctttgtga agcgactgat tggccgccga ttcagcgatg attctgtaca aaaagatata 300
aagctttggc ctttcaaaag cgtggcaggc caagaggaca ggccgatgat cgtggtgagg 360
atgaaggcg aggaaaggca gttcatgccc gaggagatct cctccatggt gctcgccaag 420
atgagggaga cggccgagggt gtacctcggc aagacggtca cgaaggccgt catcactgtc 480
ccggtctact tcaacaacgc gcagcggcag gccaccatgg acgcccggcg catcgccggc 540
ctcaacgtga tgcgcatcat caacgagccc accgccgccc ccctcgccca ctgtctcgag 600

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```

aagatgcccc tcagcaacaa ggggaggatg gtgctcgtgt tcgatctcgg tggcggcaca 660
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ggagcggatt tcgacaacga gttggtgaag cactccttgc gagagttcaa tcggaacat 780
gggtcgatgg acattgaaag caatcagaag gcattaagga gattgaggac cgcctgcgag 840
agagcgaaga ggatgctgtc atccacgatg cagaccacca ttgaggtaga ctgctccat 900
caaggcatcg acttccgcgt caccctcacc cgatcccgat ttgaggagct gaacaaggat 960
ctcttcagca agtgcattga ggctatggag aattgcctcc gcgacgcaa ggtggacaag 1020
tggagtgttg acgatgtcgt cctcgtgggt ggctccacc gcataccaa ggtgcagaag 1080
atgctgagtg agttcttga cggaaggag ctctgccgca gcatcaacc cgatgaagcc 1140
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agcggacggc tgaaccagga ggaaatcgat cgcatggctc tggagcccga gaggcacaag 1620
atgaagcga tcaagcttca cgaagtagtc taa 1653

```

<210> 46
 <211> 1437
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> line 1C-109-35 coding sequence

```

<400> 46
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gcggactggc tgaacaaggg ggacaacgag tggcagctgg tggcggcgac gctgggtgggg 120
ctgcagagcg tgccgggctt ggtggtgctg tacggcgcg tggtgaagaa gaagtgggag 180
gtgaactcgg cgttcatggc gctctacgcc ttccgcccgg tgtggatctg ctgggtcacc 240
tgggcgtaca acatgtcgtt cggggagaaag ctctccccga tctgggggaa ggcgcgccg 300
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gccgacggca gcgtggagac ggcggcggtg gagccgctgt acccgatggc gacgggtggg 420
tacttccagt gcgtgttcgc cgccatcacc ctcatcctcg tcgccggctc cctcctcggc 480
cgcatgagct tcctcgctg gatgatcttc gtcccgctct ggctcacctt ctctacacc 540
gtcggcgctt tctccctctg gggcggcggc ttctcttcc actggggcgt catcgactac 600
tgccggcggt acgtcatcca cgtctccgcc ggcatcgccg gcttcaccgc cgcttactgg 660
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gaggtcggcg acgacgccgt ccacggcgag gaggcctacg cgctctgggg cgacggcgag 1380
atgtacgacg tcaccaagca cggctccgac gccgcccgtt ccccgtcgt cgtatga 1437

```

<210> 47
 <211> 6534
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)

<223> line 1C-109-51 coding sequence

<400> 47

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<211> 543

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-056-07 coding sequence

<400> 48

```

atggttggct gccttgctac atctaccaag accatttttg cagagtctct actccacgga 60
taciaatttg acattaacac agtgacttac atggcaccct ttgccaccat gatactggct 120
ctaccagcag tgttacttga aggaggcggg gtggttacct ggttctacac acatgactcc 180
attgcttctg cactagttat catcataggc tctggagtgc ttgcattttg cctaaacttc 240

```


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```

tccatttttct acgtgatcca ttcaaccact gcagtgacct tcaatgttgc tggcaacctg 300
aaagtgtgctg ttgctgtatt ggtgtcatgg ttgatcttcc ggaaccctat ctctcctatg 360
aatgcaatcg gatgcgcgat cacgctcggt ggctgtactt tttatgggta tgtgaggcat 420
ttgatctctc aacagcaggc tgtagctcca ggaacaggaa gcccaacaac atcgcaaaaa 480
aattcgccga gaagtcggat ggagatgctc ccccttgtag gcgacaagca agaaaagggt 540
taa 543

```

```

<210> 49
<211> 2436
<212> DNA
<213> Oryza sativa

```

```

<220>
<221> misc_feature
<222> (0)...(0)
<223> line 1C-100-32 coding sequence

```

```

<400> 49
atggagatgg agatggagga caacaaggcg ccctcgccgc catcacctat ggagtccgac 60
gtcgctgagg agaagcgcaa gagggaggac gatgcatcct cctccgctgt acttgccgcc 120
gccacaacaa ccggcggtgc ccagcaccac atgtggaaga ccagcctctg ctctctcttc 180
cgccgccgag ccgcctcttc cgccgacggc tgcagccacg gcgactcctg ccgctacgag 240
cactccgagg aggagctccg cccgcgcccc gacggcacct gggacccacac ctccgaccgc 300
gccaaagaag tccgcaaggt cgccgccgac gaggtggagg aagagggtgt caccattgac 360
gacaaggccc tggacaagtg cctcgtcggc ctcccgaggg gatgggccaac cgacaggctc 420
aagactttcc tccaagacaa ggcaagaact aactactcct ccattcttcc tcctgctcta 480
ctactaggaa tctcgtatgc aacagcgaag aagaagaagg gaatgactgt tggttttgta 540
acttttgaaa atattgaaca gctgaagaat gctatcgagg tacttacaga gaaccaatct 600
ggtggaaagg aaataaagat agcagatgcc aatcgtagat ctcatcaaaa gctgcacaca 660
gaaaagcctg tatctgacaa tggagtgaac acagaaaatg gtactagtgt tgatgttcct 720
cctgggggag catctgcacc tgaagcagca atatcaaaata aaaaaagtgt ccgcatgca 780
gttactcccc ttgcccacat gtcttataat gatcagctag agcacaaaaa taattctgtt 840
gcgcagatac tgaagaggct tactcgcaat gctaggaaag cttgccctac tggcattccc 900
cttcagattt gggtttttaa atccaaagaa atttttcatt tattccattt ttcctcttta 960
gtttgtcatg attatatatt aaatcatgca ggtggctctt cttgcaagct tgaaggcatt 1020
ctggagtccc cagtgattaa tggataccgt aacaagtgtg aattctctgt gggattttct 1080
ttggagggaa aaaagcgggt tggatttatg cttggaaatt ttactgatat gattgacaaa 1140
acaaaatcca gggaagggtg gactgctgtt gaggaacctg tggactgccc aaatgtctca 1200
gaaatttcct gcaaatatgc tctgatgttc caagactttc tgcagtcac aagcttgctc 1260
gtgtggaaca gagttaataa ttgtggattt tggcgtaaat tcacagttcg ggagggaaga 1320
tgtcgagctc aagctgttgc acagaatgca gaaacccaaa tatcagaagt catgcttatt 1380
gttcaggttt gctccacagg tgttgatgat gcagtaatga aagatgaatt tgacaagttg 1440
accgttgccc tgcaacaagg agcagcaaca tgctcacctc cattacctct aacaactata 1500
gtagtgcaag atcacaaagg aatttcaaat gctgcaccag ctgattgtcc attgatccca 1560
ctattggtgc caaaagtaga tcaatcagaa ggtacagtgg ataaaacaag aatccatgac 1620
cacatcggtg atctgtggtt ctccatatca ccaacagcat tttttcagggt caatactctc 1680
gctgcagaaa gattgtatac ccttgctggt gattgggcca acctcaattc gggcacatta 1740
ctttttgacg tatgttggtg aacaggaaca attggactga ccttggcaca ccgtgttgaa 1800
atgggtgttg gaatcgaaat gaatgaatca gcagtttctg atgctgagag aaatgcgctc 1860
attaacgggtg tatcaaattg tgcgtttgtc tgtgggaagg ccgaagatgt gatggggtct 1920
cttctcactg aatatcttgg ttcaccgcag caggacattc ctgtttctga aggtgcagta 1980
agtggtagtg tgaaagatga ggaagttatt gacagttcta agaatagtgg cgaaaatttg 2040
gacagctcaa tgcagaaaaa tgacaatggc aaaagccagc agctcgggga tgcaccagct 2100
gattcttcct cttctgccat agatgagata aaggggaatt ccaatgatag gggttggaat 2160
gggttggaag gcagccatga tgaatacaat gaggttgctg gagaagatat tcatggggaa 2220
gcatcattga tcaatgagtc tgttgacctg aaagtatcgg actgtttgga ggacagaaag 2280
acatctgatg atggttcttc catttctaac aatgatgtga ctgcagctac tgcattgctcag 2340
ttcgaagaca ttgttgctat tgtggatcct cctcggtgtg ggcttcaccc tactgtaaac 2400
cccaaaagag gacagggagt tcctgttttc atttaa 2436

```

```

<210> 50
<211> 429
<212> DNA

```

<213> *Oryza sativa*

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-142-27 coding sequence

<400> 50

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atggcaatgg cttacaagat ggcgacggag gggatgaacg tgaaggagga gtgccagagg 60
tggttcatgg agatgaagtg gaagaagggtg caccgggttcg tgggtgtacaa gatcgacgag 120
cggtcgcgcg ccgtgctggt ggacaagggtg ggcggcccccg gcgaagggtta cgaggagctc 180
gtcgccgcgc tccccaccga cgactgccgc tacgccgtct tcgacttcga cttcgtcacc 240
gtcgacaact gccagaagag caagatcttc ttcatcgcct caccgaccgc atcgaggata 300
agagccaaga ttctgtacgc gacgtcgaag caagggtgta ggcgggtgct tgacggggtc 360
cactacgagg tgcaagccac ggactcctcc gagatgggtt acgacgtcat ccgaggccgc 420
gctcagtga                                     429
```

<210> 51

<211> 1344

<212> DNA

<213> *Oryza sativa*

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-140-04 coding sequence

<400> 51

```
atggcgaccg gagagctcgc tctcgtgtcc tcgctgttca tcgtcgtcgt gttcctcttg 60
cttggtgctg tggcgagaga ggcttctgcg ctcacccggc atgacttccc cgagggttc 120
gtcttcggcg caggctcctc cgctttccag gtggaagggg cagctgcaga ggatgggagg 180
aagcccagca ttitgggacac cttcatccat caatacatgc ctgacggctc caatgcagat 240
gtctcagcag atcagtatca ccattacaag gaggatgtaa agcttatgta tgacatgggg 300
ctggatgcgt acagattttc cattgcttgg cctcgtctta ttccgggaag aggagagatc 360
aacccaagg gcttggagta ctacaacaat ctgatagacg aattgataat gcatatacaa 420
cctcatgtca ccatctacca ttttgatctc cctcaggccc ttcaggatga gtatggtgga 480
atactcagcc ccagattcga agattactcg gcttatgccg aggtgtgctt caagaacttc 540
ggtgacaggg tgaagcactg ggccaccttt aaccagccga acatcgagcc catcggcggc 600
ttcgacggcg gcgaccggcc gccgcggcgg tgctcctacc ccttcggcac caactgcacc 660
ggcggcgact cctcgacgga gccgtacatc gtggctcacc acctgctgct cgctcatgcc 720
tcggcagtgt ccatctacag acagaaatac cagcaggcaa ttcaaggagg ccagataggg 780
atactctca tggttcggtg gcatgagcca tacaccgaca aaacagccga tgcagctgct 840
gccattagga tgaatgaatt ccatattgga tttttgcatc ctttggtgca cggagactac 900
cctccggtga tgaggagtcg cgtgggcggg cggttgccat ccataacggc gtcagattca 960
gagaaaatac gcggatcggt cgacttcacg ggcatcaacc attactacgt tatctttgtg 1020
caatccatcg acgcgaatga gcagaaacta cgggactact acatcgacgc aggtgttcaa 1080
gaagacgaca aggagaacat tcagtgtcat tcttggcttc ttggcaagggt gctgaatcac 1140
ctgaaactcg agtatggcaa cccccggtc atgatccacg aaatggtagt tattcagatt 1200
caccggatat cttcggaaaag atcaactaca acgatgactt cagatcggag ttcttgcagg 1260
gctacctgga agctctgtat ttgtccgtac ggtgcgctca ctctccttgc tacttacttc 1320
ctttgtgctg gtaaaggaag ttga                                     1344
```

<210> 52

<211> 223

<212> PRT

<213> *Oryza sativa*

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1B-115-22 polypeptide sequence

<400> 52

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```

Met Ala Lys Leu Ile Leu Ala Thr Phe Ala Val Val Phe Met Ala Leu
1      5      10      15
Ala Ala Thr Ser Leu Ala Gly Asp Pro Asp Met Leu Gln Asp Val Cys
20      25      30
Val Ala Asp Tyr Lys Ser Leu Lys Gly Pro Leu Arg Leu Asn Gly Phe
35      40      45
Pro Cys Lys Arg Ile Glu Asn Val Thr Ala Asn Asp Phe Phe Phe Asp
50      55      60
Gly Leu Met Lys Ala Gly Asn Thr Gly Asn Ala Val Gly Ser Val Val
65      70      75      80
Thr Ala Ala Ser Val Glu Ser Leu Pro Gly Leu Asn Thr Met Gly Val
85      90      95
Ser Met Ala Arg Ile Asp Tyr Ala Pro Trp Gly Leu Asn Pro Pro His
100     105     110
Thr His Pro Arg Ala Thr Glu Ile Ile Phe Val Val Glu Gly Ser Leu
115     120     125
Asp Val Gly Phe Val Thr Thr Ala Asn Lys Leu Phe Thr Arg Thr Val
130     135     140
Cys Lys Gly Glu Val Phe Val Phe Pro Arg Gly Leu Val His Phe Gln
145     150     155     160
Lys Asn Asn Gly Asn Thr Pro Ala Phe Ala Ile Ala Ala Leu Asn Ser
165     170     175
Gln Leu Pro Gly Thr Gln Ser Ile Ala Ala Ala Leu Phe Gly Ala Ala
180     185     190
Pro Pro Leu Pro Ser Asp Thr Leu Ala Arg Ala Phe Gln Val Asp Gly
195     200     205
Gly Met Val Glu Phe Ile Lys Ser Lys Phe Val Pro Pro Lys Tyr
210     215     220

```

<210> 53
 <211> 332
 <212> PRT
 <213> Oryza sativa

<220>
 <221> PEPTIDE
 <222> (0)...(0)
 <223> line 18-164-43 polypeptide sequence

```

<400> 53
Met Ser Ser Arg Met Ala Gly Ser Ala Ile Leu Arg His Val Gly Gly
1      5      10      15
Val Arg Leu Phe Thr Ala Ser Ala Thr Ser Pro Ala Ala Ala Ala Ala
20      25      30
Ala Ala Ala Arg Pro Phe Leu Ala Gly Gly Glu Ala Val Pro Gly Val
35      40      45
Trp Gly Leu Arg Leu Met Ser Thr Ser Ser Val Ala Ser Thr Glu Ala
50      55      60
Ala Ala Lys Ala Glu Ala Lys Lys Ala Asp Ala Glu Lys Glu Val Val
65      70      75      80
Val Asn Ser Tyr Trp Gly Ile Glu Gln Ser Lys Lys Leu Val Arg Glu
85      90      95
Asp Gly Thr Glu Trp Lys Trp Ser Cys Phe Arg Pro Trp Glu Thr Tyr
100     105     110
Thr Ala Asp Thr Ser Ile Asp Leu Thr Lys His His Val Pro Lys Thr
115     120     125
Leu Leu Asp Lys Ile Ala Tyr Trp Thr Val Lys Ser Leu Arg Phe Pro
130     135     140
Thr Asp Ile Phe Phe Gln Arg Arg Tyr Gly Cys Arg Ala Met Met Leu
145     150     155     160
Glu Thr Val Ala Ala Val Pro Gly Met Val Gly Gly Met Leu Leu His
165     170     175

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Leu Arg Ser Leu Arg Arg Phe Glu Gln Ser Gly Gly Trp Ile Arg Thr
 180 185 190
 Leu Leu Glu Glu Ala Glu Asn Glu Arg Met His Leu Met Thr Phe Met
 195 200 205
 Glu Val Ala Asn Pro Lys Trp Tyr Glu Arg Ala Leu Val Ile Thr Val
 210 215 220
 Gln Gly Val Phe Phe Asn Ala Tyr Phe Leu Gly Tyr Leu Leu Ser Pro
 225 230 235 240
 Lys Phe Ala His Arg Val Val Gly Tyr Leu Glu Glu Glu Ala Ile His
 245 250 255
 Ser Tyr Thr Glu Phe Leu Lys Asp Leu Glu Ala Gly Lys Ile Asp Asn
 260 265 270
 Val Pro Ala Pro Ala Ile Ala Ile Asp Tyr Trp Arg Leu Pro Ala Asn
 275 280 285
 Ala Thr Leu Lys Asp Val Val Thr Val Val Arg Ala Asp Glu Ala His
 290 295 300
 His Arg Asp Val Asn His Phe Ala Ser Asp Ile His Tyr Gln Gly Met
 305 310 315 320
 Glu Leu Lys Gln Thr Pro Ala Pro Ile Gly Tyr His
 325 330

<210> 54

<211> 1073

<212> PRT

<213> Oryza sativa

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1B-192-40 polypeptide sequence

<400> 54

Met Val Cys Ala Ala Ile His Ile Ala Val Val Ala Met Leu Val Ser
 1 5 10 15
 Leu Thr Ala Leu Ala Ile Ala Asp Glu Ser Asp Asn Asn Gln Arg Glu
 20 25 30
 Ala Leu Leu Cys Ile Lys Ser His Leu Ser Ser Pro Glu Gly Gly Ala
 35 40 45
 Leu Thr Thr Trp Asn Asn Thr Ser Leu Asp Met Cys Thr Trp Arg Gly
 50 55 60
 Val Thr Cys Ser Ser Glu Leu Pro Lys Pro Arg Leu Val Val Ala Leu
 65 70 75 80
 Asp Met Glu Ala Gln Gly Leu Ser Gly Glu Ile Pro Pro Cys Ile Ser
 85 90 95
 Asn Leu Ser Ser Leu Thr Arg Ile His Leu Pro Asn Asn Gly Leu Ser
 100 105 110
 Gly Gly Leu Ala Ser Ala Ala Asp Val Ala Gly Leu Arg Tyr Leu Asn
 115 120 125
 Leu Ser Phe Asn Ala Ile Gly Gly Ala Ile Pro Lys Arg Leu Gly Thr
 130 135 140
 Leu Arg Asn Leu Ser Ser Leu Asp Leu Thr Asn Asn Asn Ile His Gly
 145 150 155 160
 Glu Ile Pro Pro Leu Gly Ser Ser Ser Ala Leu Glu Ser Val Gly
 165 170 175
 Leu Ala Asp Asn Tyr Leu Thr Gly Gly Ile Pro Leu Phe Leu Ala Asn
 180 185 190
 Ala Ser Ser Leu Arg Tyr Leu Ser Leu Lys Asn Asn Ser Leu Tyr Gly
 195 200 205
 Ser Ile Pro Ala Ala Leu Phe Asn Ser Ser Thr Ile Arg Glu Ile Tyr
 210 215 220
 Leu Gly Glu Asn Asn Leu Ser Gly Ala Ile Pro Pro Val Thr Ile Phe
 225 230 235 240

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Pro	Ser	Gln	Ile	Thr	Asn	Leu	Asp	Leu	Thr	Thr	Asn	Ser	Leu	Thr	Gly
				245					250					255	
Gly	Ile	Pro	Pro	Ser	Leu	Gly	Asn	Leu	Ser	Ser	Leu	Thr	Ala	Leu	Leu
			260					265					270		
Ala	Ala	Glu	Asn	Gln	Leu	Gln	Gly	Ser	Ile	Pro	Asp	Phe	Ser	Lys	Leu
		275					280					285			
Ser	Ala	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	Tyr	Asn	Asn	Leu	Ser	Gly	Thr
	290					295				300					
Val	Asn	Pro	Ser	Val	Tyr	Asn	Met	Ser	Ser	Ile	Thr	Phe	Leu	Gly	Leu
305					310					315					320
Ala	Asn	Asn	Asn	Leu	Glu	Gly	Ile	Met	Pro	Pro	Gly	Ile	Gly	Asn	Thr
				325					330					335	
Leu	Pro	Asn	Ile	Gln	Val	Leu	Ile	Met	Ser	Asp	Asn	His	Phe	His	Gly
			340					345					350		
Glu	Ile	Pro	Lys	Ser	Leu	Ala	Asn	Ala	Ser	Asn	Met	Gln	Phe	Leu	Tyr
		355					360					365			
Leu	Ala	Asn	Asn	Ser	Leu	Arg	Gly	Val	Ile	Pro	Ser	Phe	Gly	Leu	Met
	370					375					380				
Thr	Asp	Leu	Arg	Val	Val	Met	Leu	Tyr	Ser	Asn	Gln	Leu	Glu	Ala	Gly
385					390					395					400
Asp	Trp	Ala	Phe	Leu	Ser	Ser	Leu	Lys	Asn	Cys	Ser	Asn	Leu	Gln	Lys
				405					410					415	
Leu	His	Phe	Gly	Glu	Asn	Asn	Leu	Arg	Gly	Asp	Met	Pro	Ser	Ser	Val
			420					425					430		
Ala	Glu	Leu	Pro	Lys	Thr	Leu	Thr	Ser	Leu	Ala	Leu	Pro	Ser	Asn	Tyr
		435					440					445			
Ile	Ser	Gly	Thr	Ile	Pro	Leu	Glu	Ile	Gly	Asn	Leu	Ser	Ser	Ile	Ser
	450					455					460				
Leu	Leu	Tyr	Leu	Gly	Asn	Asn	Leu	Leu	Thr	Gly	Ser	Ile	Pro	His	Thr
465					470					475					480
Leu	Gly	Gln	Leu	Asn	Asn	Leu	Val	Val	Leu	Ser	Leu	Ser	Gln	Asn	Ile
				485					490					495	
Phe	Ser	Gly	Glu	Ile	Pro	Gln	Ser	Ile	Gly	Asn	Leu	Asn	Arg	Leu	Thr
			500					505					510		
Glu	Leu	Tyr	Leu	Ala	Glu	Asn	Gln	Leu	Thr	Gly	Arg	Ile	Pro	Ala	Thr
		515					520					525			
Leu	Ser	Arg	Cys	Gln	Gln	Leu	Leu	Ala	Leu	Asn	Leu	Ser	Cys	Asn	Ala
	530					535					540				
Leu	Thr	Gly	Ser	Ile	Ser	Gly	Asp	Met	Phe	Ile	Lys	Leu	Asn	Gln	Leu
545					550					555					560
Ser	Trp	Leu	Leu	Asp	Leu	Ser	His	Asn	Gln	Phe	Ile	Asn	Ser	Ile	Pro
				565					570					575	
Leu	Glu	Leu	Gly	Ser	Leu	Ile	Asn	Leu	Ala	Ser	Leu	Asn	Ile	Ser	His
			580					585					590		
Asn	Lys	Leu	Thr	Gly	Arg	Ile	Pro	Ser	Thr	Leu	Gly	Ser	Cys	Val	Arg
		595					600					605			
Leu	Glu	Ser	Leu	Arg	Val	Gly	Gly	Asn	Phe	Leu	Glu	Gly	Ser	Ile	Pro
	610					615					620				
Gln	Ser	Leu	Ala	Asn	Leu	Arg	Gly	Thr	Lys	Val	Leu	Asp	Phe	Ser	Gln
625					630					635					640
Asn	Asn	Leu	Ser	Gly	Ala	Ile	Pro	Asp	Phe	Phe	Gly	Thr	Phe	Thr	Ser
				645					650					655	
Leu	Gln	Tyr	Leu	Asn	Met	Ser	Tyr	Asn	Asn	Phe	Glu	Gly	Pro	Ile	Pro
			660					665					670		
Val	Asp	Gly	Ile	Phe	Ala	Asp	Arg	Asn	Lys	Val	Phe	Val	Gln	Gly	Asn
		675					680					685			
Pro	His	Leu	Cys	Thr	Asn	Val	Pro	Met	Asp	Glu	Leu	Thr	Val	Cys	Ser
	690					695					700				
Ala	Ser	Ala	Ser	Lys	Arg	Lys	Asn	Lys	Leu	Ile	Ile	Pro	Met	Leu	Ala
705					710					715					720
Ala	Phe	Ser	Ser	Ile	Ile	Leu	Leu	Ser	Ser	Ile	Leu	Gly	Leu	Tyr	Phe
				725					730					735	
Leu	Ile	Val	Asn	Val	Phe	Leu	Lys	Arg	Lys	Trp	Lys	Ser	Asn	Glu	His

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Met	Asp	His	740	Thr	Tyr	Met	Glu	Leu	745	Lys	Thr	Leu	Thr	Tyr	750	Ser	Asp	Val
Ser	Lys	Ala	755	Thr	Asn	Asn	Phe	Ser	760	Ala	Ala	Asn	Ile	Val	765	Gly	Ser	Gly
His	Phe	Gly	770	Thr	Val	Tyr	Arg	Gly	775	Ile	Leu	His	Thr	Glu	780	Asp	Thr	Met
785	Val	Ala	Val	Lys	Val	805	Phe	Lys	Leu	Asp	Gln	Cys	Gly	Ala	Leu	Asp	800	Ser
Phe	Met	Ala	Glu	Cys	Lys	Ala	Leu	Lys	810	Asn	Ile	Arg	His	Arg	Asn	Leu	815	
Val	Lys	Val	820	Ile	Thr	Ala	Cys	Ser	825	Thr	Tyr	Asp	Pro	Met	Gly	Ser	Glu	
Phe	Lys	Ala	835	Leu	Val	Phe	Glu	Tyr	840	Met	Ala	Asn	Gly	Ser	Leu	Glu	Ser	
850	Arg	Leu	His	Thr	Lys	Phe	Asp	Arg	855	Cys	Gly	Asp	Leu	Ser	Leu	Gly	Glu	
865	Arg	Ile	Ser	Ile	Ala	870	Phe	Asp	Ile	Ala	875	Ser	Ala	Leu	Glu	Tyr	Leu	His
Asn	Gln	Cys	885	Ile	Pro	Pro	Val	Val	890	His	Cys	Asp	Leu	Lys	Pro	Ser	Asn	
Val	Leu	Phe	900	Asn	Asn	Asp	Asp	Val	905	Ala	Cys	Val	Cys	Asp	Phe	Gly	Leu	
Ala	Arg	Ser	915	Ile	Arg	Val	Tyr	Ser	920	Ser	Ser	Gly	Thr	Gln	Ser	Ile	Ser	Thr
930	Ser	Met	Ala	Gly	Pro	Arg	Gly	Ser	935	Ile	Gly	Tyr	Ile	Ala	Pro	Glu	Tyr	
945	Gly	Met	Gly	Ser	Gln	Ile	Ser	Thr	950	Glu	Gly	Asp	Val	Tyr	Ser	Tyr	Gly	
Ile	Ile	Leu	965	Leu	Glu	Met	Leu	Thr	970	Gly	Arg	His	Pro	Thr	Asn	Glu	Ile	
Phe	Thr	Asp	980	Gly	Leu	Thr	Leu	Arg	985	Met	Tyr	Val	Asn	Ala	Ser	Leu	Ser	
Gln	Ile	Lys	995	Asp	Ile	Leu	Asp	Pro	1000	Arg	Leu	Ile	Pro	Glu	Met	Thr	Glu	
1010	Gln	Pro	Ser	Asn	His	Thr	Leu	Gln	1015	Leu	His	Glu	His	Lys	Lys	Thr	Val	
1025	Pro	Ser	Arg	Cys	Lys	1030	Leu	Gly	Gly	Val	Glu	Gly	Ile	Leu	Thr	Cys	Thr	
Ile	Arg	Glu	1045	Ile	Ala	Ser	Lys	Leu	1050	Gly	Gly	Leu	Arg	Leu	Ser	Met	Leu	
Thr			1060						1065						1070			

<210> 55
 <211> 637
 <212> PRT
 <213> Oryza sativa

<220>
 <221> PEPTIDE
 <222> (0)...(0)
 <223> line 1B-207-27 polypeptide sequence

<400> 55
 Met Gln Asp His Ile Leu Thr Ala Phe Leu Val Val Ser Leu Leu Phe
 1 5 10 15
 Ala Cys Ile Pro Ala Lys Ser Ala Asp Leu Asn Ser Asp Lys Gln
 20 25 30
 Ala Leu Leu Ala Phe Ala Ala Ser Leu Pro His Gly Arg Lys Leu Asn
 35 40 45
 Trp Ser Ser Ala Ala Pro Val Cys Thr Ser Trp Val Gly Val Thr Cys

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50	Thr	Pro	Asp	Asn	Ser	Arg	Val	Gln	Thr	Leu	Arg	Leu	Pro	Ala	Val	Gly
65	Leu	Phe	Gly	Pro	Leu	Pro	Ser	Asp	Thr	Leu	Gly	Lys	Leu	Asp	Ala	Leu
				85	Leu	Arg	Ser	Asn	Arg	Ile	Thr	Val	Asp	Leu	Pro	Pro
	Glu	Val	Leu	Ser	Leu	Arg	Ser	Asn	Arg	Ile	Thr	Val	Asp	Leu	Pro	Pro
				100					105					110		
	Glu	Val	Gly	Ser	Ile	Pro	Ser	Leu	His	Ser	Leu	Tyr	Leu	Gln	His	Asn
				115					120					125		
	Asn	Leu	Ser	Gly	Ile	Ile	Pro	Thr	Ser	Leu	Thr	Ser	Thr	Leu	Thr	Phe
				130					135					140		
	Leu	Asp	Leu	Ser	Tyr	Asn	Thr	Phe	Asp	Gly	Glu	Ile	Pro	Leu	Arg	Val
																160
	Gln	Asn	Leu	Thr	Gln	Leu	Thr	Ala	Leu	Leu	Gln	Asn	Asn	Ser	Ser	Leu
					165					170						175
	Ser	Gly	Pro	Ile	Pro	Asp	Leu	Gln	Leu	Pro	Lys	Leu	Arg	His	Leu	Asn
				180						185						190
	Leu	Ser	Asn	Asn	Asn	Leu	Ser	Gly	Pro	Ile	Pro	Pro	Ser	Leu	Gln	Arg
				195					200					205		
	Phe	Pro	Ala	Asn	Ser	Phe	Leu	Gly	Asn	Ala	Phe	Leu	Cys	Gly	Phe	Pro
	Leu	Gln	Pro	Cys	Pro	Gly	Thr	Ala	Pro	Ser	Pro	Ser	Pro	Ser	Pro	Thr
																240
	Ser	Pro	Ser	Pro	Gly	Lys	Ala	Lys	Lys	Gly	Phe	Trp	Lys	Arg	Ile	Arg
					245											255
	Thr	Gly	Val	Ile	Ala	Leu	Ala	Ala	Ala	Gly	Gly	Val	Leu	Leu	Leu	Leu
				260					265					270		
	Ile	Leu	Ile	Val	Leu	Leu	Leu	Ile	Cys	Ile	Phe	Lys	Arg	Lys	Lys	Ser
				275					280					285		
	Thr	Glu	Pro	Thr	Thr	Ala	Ser	Ser	Ser	Lys	Gly	Lys	Thr	Val	Ala	Gly
	Gly	Arg	Gly	Glu	Asn	Pro	Lys	Glu	Glu	Tyr	Ser	Ser	Gly	Val	Gln	Glu
																320
	Ala	Glu	Arg	Asn	Lys	Leu	Val	Phe	Phe	Glu	Gly	Cys	Ser	Tyr	Asn	Phe
					325					330						335
	Asp	Leu	Glu	Asp	Leu	Leu	Arg	Ala	Ser	Ala	Glu	Val	Leu	Gly	Lys	Gly
	Ser	Tyr	Gly	Thr	Thr	Tyr	Lys	Ala	Val	Leu	Glu	Asp	Gly	Thr	Thr	Val
	Val	Val	Lys	Arg	Leu	Lys	Glu	Val	Val	Val	Gly	Lys	Lys	Asp	Phe	Glu
	Gln	Gln	Met	Glu	Ile	Val	Gly	Arg	Val	Gly	Gln	His	Gln	Asn	Val	Val
																400
	Pro	Leu	Arg	Ala	Tyr	Tyr	Tyr	Ser	Lys	Asp	Glu	Lys	Leu	Leu	Val	Tyr
					405					410						415
	Asp	Tyr	Ile	Pro	Ser	Gly	Ser	Leu	Ala	Val	Val	Leu	His	Gly	Asn	Lys
	Ala	Thr	Gly	Lys	Ala	Pro	Leu	Asp	Trp	Glu	Thr	Arg	Val	Lys	Ile	Ser
	Leu	Gly	Val	Ala	Arg	Gly	Ile	Ala	His	Leu	His	Ala	Glu	Gly	Gly	Gly
	Lys	Phe	Ile	His	Gly	Asn	Leu	Lys	Ser	Ser	Asn	Ile	Leu	Leu	Ser	Gln
																480
	Asn	Leu	Asp	Gly	Cys	Val	Ser	Glu	Phe	Gly	Leu	Ala	Gln	Leu	Met	Thr
					485					490						495
	Ile	Pro	Pro	Ala	Pro	Ala	Arg	Leu	Val	Gly	Tyr	Arg	Ala	Pro	Glu	Val
	Leu	Glu	Thr	Lys	Lys	Pro	Thr	Gln	Lys	Ser	Asp	Val	Tyr	Ser	Phe	Gly
	Val	Leu	Val	Leu	Glu	Met	Leu	Thr	Gly	Lys	Ala	Pro	Leu	Arg	Ser	Pro
	Gly	Arg	Glu	Asp	Ser	Ile	Glu	His	Leu	Pro	Arg	Trp	Val	Gln	Ser	Val
																560

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Val	Arg	Glu	Glu	Trp	Thr	Ala	Glu	Val	Phe	Asp	Val	Asp	Leu	Leu	Arg
				565					570					575	
His	Pro	Asn	Ile	Glu	Asp	Glu	Met	Val	Gln	Met	Leu	Gln	Val	Ala	Met
			580					585					590		
Ala	Cys	Val	Ala	Ala	Pro	Pro	Asp	Gln	Arg	Pro	Lys	Met	Asp	Glu	Val
		595					600					605			
Ile	Arg	Arg	Ile	Val	Glu	Ile	Arg	Asn	Ser	Tyr	Ser	Gly	Ser	Arg	Thr
	610					615					620				
Pro	Pro	Glu	Glu	Lys	Gln	Lys	Asp	Glu	Ser	Ala	Ala	Pro			
625					630					635					

<210> 56
 <211> 523
 <212> PRT
 <213> Oryza sativa

<220>
 <221> PEPTIDE
 <222> (0)...(0)
 <223> line 1B-138-07 polypeptide sequence

<400> 56

Met	Ala	Ala	Pro	Leu	Ser	Thr	Ala	Ala	Ala	Ala	Ser	Trp	Leu	Ser	Asp
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Ser	Ala	Ser	Ser	Pro	Pro	Arg	Val	Arg	Leu	Leu	Ile	Gly	Gly	Glu	Phe
			20					25					30		
Val	Glu	Ser	Arg	Ala	Asp	Glu	His	Val	Asp	Val	Thr	Asn	Pro	Ala	Thr
		35					40					45			
Gln	Glu	Val	Val	Ser	Arg	Ile	Pro	Leu	Thr	Thr	Ala	Asp	Glu	Phe	Arg
	50					55					60				
Ala	Ala	Val	Asp	Ala	Ala	Arg	Thr	Ala	Phe	Pro	Gly	Trp	Arg	Asn	Thr
65				70					75					80	
Pro	Val	Thr	Thr	Arg	Gln	Arg	Ile	Met	Leu	Lys	Tyr	Gln	Glu	Leu	Ile
				85				90					95		
Arg	Ala	Asn	Met	Asp	Lys	Leu	Ala	Glu	Asn	Ile	Thr	Thr	Glu	Gln	Gly
			100					105					110		
Lys	Thr	Leu	Lys	Asp	Ala	Trp	Gly	Asp	Val	Phe	Arg	Gly	Leu	Glu	Val
		115					120					125			
Val	Glu	His	Ala	Cys	Gly	Met	Gly	Thr	Leu	Gln	Met	Gly	Glu	Tyr	Val
	130				135						140				
Ser	Asn	Val	Ser	Asn	Gly	Ile	Asp	Thr	Phe	Ser	Ile	Arg	Glu	Pro	Leu
145					150				155					160	
Gly	Val	Cys	Ala	Gly	Ile	Cys	Pro	Phe	Asn	Phe	Pro	Ala	Met	Ile	Pro
			165					170					175		
Leu	Trp	Met	Phe	Pro	Ile	Ala	Val	Thr	Cys	Gly	Asn	Thr	Phe	Val	Leu
		180						185					190		
Lys	Pro	Ser	Glu	Lys	Asp	Pro	Gly	Ala	Ala	Met	Met	Leu	Ala	Glu	Leu
		195					200					205			
Ala	Met	Glu	Ala	Gly	Leu	Pro	Lys	Gly	Val	Leu	Asn	Ile	Val	His	Gly
	210					215					220				
Thr	His	Asp	Val	Val	Asn	Asn	Ile	Cys	Asp	Asp	Glu	Asp	Ile	Lys	Ala
225					230				235					240	
Val	Ser	Phe	Val	Gly	Ser	Asn	Ile	Ala	Gly	Met	His	Ile	Tyr	Ser	Arg
			245						250					255	
Ala	Ser	Ala	Lys	Gly	Lys	Arg	Val	Gln	Ser	Asn	Met	Gly	Ala	Lys	Asn
			260					265					270		
His	Ala	Ile	Ile	Leu	Pro	Asp	Ala	Asp	Arg	Asp	Ala	Thr	Leu	Asn	Ala
		275					280					285			
Leu	Ile	Ala	Ala	Gly	Phe	Gly	Ala	Ala	Gly	Gln	Arg	Cys	Met	Ala	Leu
	290					295					300				
Ser	Thr	Ala	Val	Phe	Val	Gly	Gly	Ser	Glu	Pro	Trp	Ile	Arg	Pro	Gly
305					310					315					320

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Ile Arg Glu Asp Glu Leu Val Lys Arg Ala Ser Ser Leu Val Val Asn
 325 330 335
 Ser Gly Met Ala Ser Asp Ala Asp Leu Gly Pro Val Ile Ser Lys Gln
 340 345 350
 Ala Lys Glu Arg Ile Cys Lys Leu Ile Gln Ser Gly Ala Asp Asn Gly
 355 360 365
 Ala Arg Val Leu Leu Asp Gly Arg Asp Ile Val Val Pro Asn Phe Glu
 370 375 380
 Asn Gly Asn Phe Val Gly Pro Thr Leu Leu Ala Asp Val Lys Ser Glu
 385 390 395 400
 Met Glu Cys Tyr Lys Glu Glu Ile Phe Gly Pro Val Leu Leu Leu Met
 405 410 415
 Lys Ala Glu Ser Leu Asp Asp Ala Ile Gln Ile Val Asn Arg Asn Lys
 420 425 430
 Tyr Gly Asn Gly Ala Ser Ile Phe Thr Thr Ser Gly Val Ser Ala Arg
 435 440 445
 Lys Phe Gln Thr Asp Ile Glu Ala Gly Gln Val Gly Ile Asn Val Pro
 450 455 460
 Ile Pro Val Pro Leu Pro Phe Phe Ser Phe Thr Gly Ser Lys Ala Ser
 465 470 475 480
 Phe Ala Gly Asp Leu Asn Phe Tyr Gly Lys Ala Gly Val Gln Phe Phe
 485 490 495
 Thr Gln Ile Lys Thr Val Thr Gln Gln Trp Lys Glu Ser Pro Ala Gln
 500 505 510
 Arg Val Ser Leu Ser Met Pro Thr Ser Gln Lys
 515 520

<210> 57
 <211> 446
 <212> PRT
 <213> Oryza sativa

<220>
 <221> PEPTIDE
 <222> (0)...(0)
 <223> line 1D-059-12 polypeptide sequence

<400> 57
 Met Ala Ala Ala Ala Thr Ala Ala Val Pro Leu Asp Glu Ala Lys Ala
 1 5 10 15
 Lys Glu Val Leu Arg Gln Val Glu Phe Tyr Phe Ser Asp Ser Asn Leu
 20 25 30
 Pro Arg Asp Asn Phe Leu Arg Lys Thr Val Glu Glu Ser Glu Asp Gly
 35 40 45
 Leu Val Ser Leu Ala Leu Ile Cys Ser Phe Ser Arg Met Lys Lys His
 50 55 60
 Leu Gly Leu Asp Ala Asp Val Lys Gln Glu Thr Met Pro Glu Glu Thr
 65 70 75 80
 Val Leu Ala Val Ala Glu Val Leu Arg Arg Ser Ser Ala Leu Arg Val
 85 90 95
 Thr Glu Asp Gly Lys Lys Val Gly Arg Ser Ile Glu Leu Ser Lys Leu
 100 105 110
 Asp Glu Ile Met Glu Gln Val Asp Ser Arg Thr Ile Ala Ala Ser Pro
 115 120 125
 Phe Pro Tyr Asn Val Lys Leu Glu Asp Val Gln Ser Phe Phe Ala Gln
 130 135 140
 Tyr Gly Lys Val Asn Ser Val Arg Leu Pro Arg His Ile Ala Asp Lys
 145 150 155 160
 Arg His Phe Cys Gly Thr Ala Leu Val Glu Phe Ser Glu Glu Glu Glu
 165 170 175
 Ala Asn Ala Val Leu Lys Asn Thr Leu Val Phe Ala Gly Ala Asp Leu
 180 185 190

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Glu Ile Lys Pro Lys Lys Glu Phe Asp Thr Glu Arg Glu Ala Lys Lys
 195 200 205
 Glu Ala Tyr Glu Lys Ser Gln Pro Thr Lys Asn Gly His Asp Glu Gly
 210 215 220
 Tyr Pro Lys Gly Leu Ile Val Ala Phe Lys Leu Lys Ile Ile Gln Ile
 225 230 235 240
 Asp Gly Gly Met Ala Glu Asn Gly Gly Asp Lys Glu Gly Glu Thr Asp
 245 250 255
 Asp Ala Asn Lys Ser Arg Thr Gly His Asp Glu Lys Ile Pro Glu Asn
 260 265 270
 Ser Asp Ile Lys Glu Asp Leu Ser Asp Asp Val Glu Lys Ser Lys Glu
 275 280 285
 Ala Ala Ala Gln Ser Val Lys Lys Gly Glu Ser Pro Ser Glu Asn Ala
 290 295 300
 Asp Asp Pro Ile Ser Arg Glu Asp Phe Lys Glu Glu Phe Gly Lys Phe
 305 310 315 320
 Gly Thr Val Arg Tyr Val Asp Phe Ser Ile Gly Glu Asp Ser Gly Tyr
 325 330 335
 Ile Arg Phe Glu Asp Ser Lys Ala Ala Glu Lys Ala Arg Ala Leu Ala
 340 345 350
 Ala Ile Ser Asp Glu Gly Gly Leu Ile Met Lys Gly His Leu Val Thr
 355 360 365
 Leu Glu Pro Val Ser Gly Gln Ala Glu Lys Asp Tyr Trp Ser Ala Ile
 370 375 380
 Lys Gly Gly Gln Gly Lys Tyr Arg Asp Asn Arg Ser Asn Arg Gly Arg
 385 390 395 400
 Ala Asp Pro Leu Lys Tyr His Asn Ala Pro Arg Met Asn Leu Arg Ser
 405 410 415
 Gly Leu Lys Leu Lys Ile Glu Val Glu Ala Leu Trp His Thr Arg Met
 420 425 430
 Pro Thr His Ile Phe Gly Val Ile Leu Ser Trp Asn Trp Gln
 435 440 445

<210> 58

<211> 859

<212> PRT

<213> Oryza sativa

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1C-087-40 polypeptide sequence

<400> 58

Met Ala Thr Arg Tyr Trp Ile Val Ser Leu Pro Val Gln Thr Pro Gly
 1 5 10 15
 Ser Thr Ala Asn Ser Leu Trp Ala Arg Leu Gln Asp Ser Ile Ser Arg
 20 25 30
 His Ser Phe Asp Thr Pro Leu Tyr Arg Phe Asn Val Pro Asp Leu Arg
 35 40 45
 Val Gly Thr Leu Asp Ser Leu Leu Ala Leu Ser Asp Asp Leu Val Lys
 50 55 60
 Ser Asn Val Phe Ile Glu Gly Val Ser His Lys Ile Arg Arg Gln Ile
 65 70 75 80
 Glu Glu Leu Glu Arg Ala Gly Gly Val Glu Ser Gly Ala Leu Thr Val
 85 90 95
 Asp Gly Val Pro Val Asp Thr Tyr Leu Thr Arg Phe Val Trp Asp Glu
 100 105 110
 Gly Lys Tyr Pro Thr Met Ser Pro Lys Glu Ile Val Gly Ser Ile
 115 120 125
 Gln Ser Gln Val Ser Lys Ile Glu Asp Asp Met Lys Val Arg Gly Ala
 130 135 140

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Glu	Tyr	Asn	Asn	Val	Arg	Ser	Gln	Leu	Ser	Ala	Ile	Asn	Arg	Lys	Gln
145					150					155					160
Thr	Gly	Ser	Leu	Ala	Val	Arg	Asp	Leu	Ser	Asn	Leu	Val	Lys	Pro	Glu
				165					170					175	
Asp	Met	Val	Thr	Ser	Glu	His	Leu	Val	Thr	Leu	Leu	Ala	Val	Val	Pro
			180					185					190		
Lys	Tyr	Ser	Gln	Lys	Asp	Trp	Leu	Ser	Ser	Tyr	Glu	Ser	Leu	Asp	Thr
		195					200					205			
Phe	Val	Val	Pro	Arg	Ser	Ser	Lys	Lys	Leu	Tyr	Glu	Asp	Asn	Glu	Tyr
	210					215					220				
Ala	Leu	Tyr	Thr	Val	Thr	Leu	Phe	Ala	Lys	Val	Val	Asp	Asn	Phe	Lys
225					230					235					240
Val	Arg	Ala	Arg	Glu	Lys	Gly	Phe	Gln	Val	Arg	Asp	Phe	Glu	Tyr	Ser
				245					250					255	
Ser	Glu	Ala	Gln	Glu	Ser	Arg	Lys	Glu	Glu	Leu	Glu	Lys	Leu	Met	Gln
			260					265					270		
Asp	Gln	Glu	Ala	Met	Arg	Ala	Ser	Leu	Leu	Gln	Trp	Cys	Tyr	Ala	Ser
		275					280					285			
Tyr	Ser	Glu	Asn	Thr	Ile	Tyr	Val	Arg	His	Ala	Lys	Val	Gln	Asn	Phe
	290					295					300				
Val	Leu	Leu	Tyr	Val	Phe	Ser	Ser	Trp	Met	His	Phe	Cys	Ala	Val	Arg
305					310					315					320
Val	Phe	Val	Glu	Ser	Ile	Leu	Arg	Tyr	Gly	Leu	Pro	Pro	Ser	Phe	Leu
				325					330					335	
Ser	Ala	Val	Leu	Ala	Pro	Ser	Gln	Lys	Gly	Glu	Lys	Lys	Val	Arg	Ser
			340					345					350		
Ile	Leu	Glu	Glu	Leu	Cys	Gly	Asn	Val	His	Ser	Ile	Tyr	Trp	Lys	Ser
		355					360					365			
Glu	Asp	Asp	Val	Gly	Val	Ala	Gly	Leu	Gly	Glu	His	Arg	Val	Arg	Cys
	370					375					380				
Cys	Gly	Tyr	Tyr	Val	Phe	Val	Thr	Leu	Ser	Ser	Gln	Lys	Asp	Lys	Leu
385					390					395					400
Gly	Val	Met	Tyr	Arg	Thr	Ser	Ile	Leu	Gly	Asp	Pro	Val	Pro	Thr	Asp
				405					410					415	
Asp	Ser	Arg	Val	Asp	Lys	Thr	Gln	Glu	Glu	Met	Met	Val	Lys	Glu	Lys
			420					425					430		
Glu	Ile	His	Val	Met	Ser	Asn	Arg	Arg	Lys	Arg	Gly	Glu	Ser	Lys	
		435					440				445				
Pro	Gln	Ala	His	Asp	Ala	Gly	Asp	Thr	Thr	Pro	Ile	Asp	Asn	Ile	Leu
	450					455					460				
Thr	Ser	Leu	Asp	Asp	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Arg	Arg	Glu
465					470					475					480
Leu	Pro	Leu	Leu	Gln	Leu	Asn	Asp	His	Gln	Glu	Ala	Asp	Asp	Ala	Asp
				485					490					495	
Ala	Ser	Ser	Ser	Ser	Ser	Pro	His	Gln	Gln	Arg	Arg	Leu	Trp	Val	Lys
				500				505					510		
Asp	Arg	Ser	Arg	Ala	Trp	Trp	Glu	Leu	Cys	Ser	Ser	Ala	Asp	Tyr	Pro
		515					520					525			
Glu	Ala	Asp	Phe	Arg	Arg	Ala	Phe	Arg	Met	Ser	Arg	Pro	Thr	Phe	His
	530					535					540				
Phe	Leu	Cys	Asp	Ala	Leu	Ala	Ala	Ala	Val	Ala	Lys	Glu	Asp	Thr	Ala
545					550					555					560
Leu	Arg	Ala	Ala	Ile	Pro	Val	Arg	Gln	Arg	Val	Ala	Val	Cys	Val	Trp
				565					570					575	
Arg	Leu	Ala	Thr	Gly	Glu	Pro	Leu	Arg	Val	Val	Ser	Lys	Arg	Phe	Gly
			580					585					590		
Leu	Gly	Ile	Ser	Thr	Cys	His	Lys	Leu	Ile	Leu	Glu	Val	Cys	Ala	Ala
		595					600					605			
Ile	Arg	Asn	Leu	Leu	Met	Pro	Arg	Phe	Leu	His	Trp	Pro	Asp	His	Pro
	610					615					620				
Thr	Ser	Thr	Ala	Tyr	Lys	Thr	Arg	Phe	Glu	Ala	Thr	Ser	Gly	Val	Ser
625					630					635					640
Gly	Val	Val	Gly	Ala	Met	Tyr	Thr	Thr	His	Ile	Pro	Ile	Ile	Ala	Pro

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0403A.5125															
				645				650				655			
Lys	Val	Ser	Val	Ala	Ala	Tyr	Leu	Asn	Arg	Arg	His	Thr	Glu	Arg	Asn
660				665				670				675			
His	Lys	Thr	Ser	Tyr	Ser	Ile	Thr	Leu	Gln	Gly	Val	Val	Gly	Pro	Asp
675				680				685				690			
Gly	Thr	Phe	Thr	Asp	Val	Cys	Ile	Gly	Trp	Pro	Gly	Ser	Met	Ser	Asp
690				695				700				705			
Glu	Gln	Val	Leu	Arg	Lys	Ser	Ala	Leu	His	Gln	Arg	Ala	Ser	Ala	Ala
705				710				715				720			
Ala	Gly	Ser	Met	Ser	Trp	Val	Val	Gly	Gly	Ala	Ser	Tyr	Pro	Leu	Thr
725				730				735				740			
Glu	Trp	Met	Leu	Val	Pro	Tyr	Ala	Gln	Arg	Asn	Leu	Thr	Trp	Thr	Gln
740				745				750				755			
His	Ala	Phe	Asn	Glu	Lys	Val	Gly	Glu	Val	Arg	Arg	Val	Ala	Thr	Glu
755				760				765				770			
Ala	Phe	Val	Arg	Leu	Lys	Gly	Arg	Trp	Ala	Cys	Leu	Gln	Lys	Arg	Thr
770				775				780				785			
Glu	Val	Lys	Leu	Gln	Asp	Leu	Pro	Ala	Val	Leu	Ala	Ala	Cys	Cys	Val
785				790				795				800			
Leu	His	Asn	Ile	Cys	Glu	Thr	Arg	Gly	Glu	Asp	Met	Asp	Pro	Asp	Leu
805				810				815				820			
Arg	Cys	Asp	Leu	Pro	Pro	Asp	Glu	Glu	Glu	Asp	Asp	Thr	Val	Leu	Val
820				825				830				835			
Gln	Ser	Glu	Ser	Ala	Asn	Lys	Val	Arg	Asp	Asp	Ile	Ala	His	Asn	Leu
835				840				845				850			
Leu	His	Arg	Gly	Leu	Ala	Gly	Thr	Ala	Phe	Phe					
850				855				860				865			

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<210> 59
<211> 473
<212> PRT
<213> Oryza sativa
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<220>  
<221> PEPTIDE  
<222> (0)...(0)  
<223> line 1C-017-14 polypeptide sequence
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<400>	59														
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Ala	Val	Leu	Ala	Leu	Val	Val	Ala	Lys	Leu	Thr	Gly	Lys	Arg	Leu	Arg
			20					25					30		
Leu	Pro	Pro	Gly	Pro	Ala	Gly	Ala	Pro	Ile	Val	Gly	Asn	Trp	Leu	Gln
		35					40					45			
Val	Gly	Asp	Asp	Leu	Asn	His	Arg	Asn	Leu	Met	Ala	Leu	Ala	Arg	Arg
	50					55					60				
Phe	Gly	Asp	Ile	Leu	Leu	Leu	Arg	Met	Gly	Val	Arg	Asn	Leu	Val	Val
65				70						75					80
Val	Ser	Ser	Pro	Asp	Leu	Ala	Lys	Glu	Val	Leu	His	Thr	Gln	Gly	Val
				85					90					95	
Glu	Phe	Gly	Ser	Arg	Thr	Arg	Asn	Val	Val	Phe	Asp	Ile	Phe	Thr	Gly
			100					105					110		
Lys	Gly	Gln	Asp	Met	Val	Phe	Thr	Val	Tyr	Gly	Asp	His	Trp	Arg	Lys
		115					120					125			
Met	Arg	Arg	Ile	Met	Thr	Val	Pro	Phe	Phe	Thr	Asn	Lys	Val	Val	Ala
	130					135					140				
Gln	Asn	Arg	Ala	Gly	Trp	Glu	Glu	Glu	Ala	Arg	Leu	Val	Val	Glu	Asp
145					150					155					160
Val	Arg	Arg	Asp	Pro	Thr	Ala	Ala	Thr	Ser	Gly	Val	Val	Ile	Arg	Arg
				165					170					175	
Arg	Leu	Gln	Leu	Met	Met	Tyr	Asn	Asp	Met	Phe	Arg	Ile	Met	Phe	Asp

			180					185					190		
Arg	Arg	Phe 195	Asp	Ser	Val	Asp	Asp 200	Pro	Leu	Phe	Asn 205	Lys	Leu	Lys	Ala
Phe	Asn 210	Ala	Glu	Arg	Ser	Arg 215	Leu	Ser	Gln	Ser	Phe 220	Glu	Tyr	Asn	Tyr
Gly 225	Asp	Phe	Ile	Pro	Val 230	Leu	Arg	Pro	Phe	Leu 235	Arg	Arg	Tyr	Leu	Ala 240
Arg	Cys	His	Gln	Leu 245	Lys	Ser	Gln	Arg	Met 250	Lys	Leu	Phe	Glu	Asp 255	His
Phe	Val	Gln	Glu 260	Arg	Lys	Arg	Val	Met 265	Glu	Gln	Thr	Gly	Glu 270	Ile	Arg
Cys	Ala	Met 275	Asp	His	Ile	Leu	Glu 280	Ala	Glu	Arg	Lys	Gly 285	Glu	Ile	Asn
His	Asp 290	Asn	Val	Leu	Tyr	Ile 295	Val	Glu	Asn	Ile	Asn 300	Val	Ala	Ala	Ile
Glu 305	Thr	Thr	Leu	Trp	Ser 310	Ile	Glu	Trp	Gly	Ile 315	Ala	Glu	Leu	Val	Asn 320
His	Pro	Ser	Ile 325	Gln	Ser	Lys	Val	Arg	Glu 330	Glu	Met	Ala	Ser	Val 335	Leu
Gly	Gly	Ala	Ala 340	Val	Thr	Glu	Pro	Asp 345	Leu	Glu	Arg	Leu	Pro 350	Tyr	Leu
Gln	Ala	Val 355	Val	Lys	Glu	Thr	Leu 360	Arg	Leu	Arg	Met	Ala 365	Ile	Pro	Leu
Leu	Val 370	Pro	His	Met	Asn	Leu 375	Ala	Asp	Gly	Lys	Leu 380	Ala	Gly	Tyr	Asp
Ile 385	Pro	Ala	Glu	Ser	Lys 390	Ile	Leu	Val	Asn	Ala 395	Trp	Phe	Leu	Ala	Asn 400
Asp	Pro	Lys	Arg	Trp 405	Val	Arg	Pro	Asp	Glu 410	Phe	Arg	Pro	Glu	Arg 415	Phe
Leu	Glu	Glu	Glu 420	Lys	Ala	Val	Glu	Ala 425	His	Gly	Asn	Asp	Phe 430	Arg	Phe
Val	Pro	Phe 435	Gly	Val	Gly	Arg	Arg 440	Ser	Cys	Pro	Gly	Ile 445	Ile	Leu	Ala
Leu	Pro 450	Ile	Ile	Gly	Ile	Thr 455	Leu	Gly	Arg	Leu	Val 460	Gln	Ser	Phe	Asp
Leu 465	Leu	Pro	Pro	Pro	Gly 470	Met	Asp	Lys							

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<210> 60
<211> 408
<212> PRT
<213> Oryza sativa
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<220>  
<221> PEPTIDE  
<222> (0)...(0)  
<223> line 1C-038-56 polypeptide sequence
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<400>	60															
Asp	Val	Gln	Gln	His	Ser	Gly	Ser	Ser	Ser	Ser	Ser	Thr	Glu	Ser	Asp	
1				5					10					15		
Val	Gln	Glu	Thr	Ala	Ala	Val	Ala	Val	Ala	Asp	Pro	Ser	Pro	Arg	Ser	
			20					25					30			
Glu	Val	Val	Asp	Gly	Glu	Ser	Pro	Pro	Gln	Pro	Gly	Gly	Glu	Ala	Ala	
		35					40					45				
Ser	His	Gln	Gln	Gln	Gln	Lys	Glu	Met	Lys	Leu	Lys	Lys	Pro	Asp	Lys	
	50					55					60					
Ile	Leu	Pro	Cys	Pro	Arg	Cys	Ser	Ser	Met	Asp	Thr	Lys	Phe	Cys	Tyr	
65					70					75					80	
Phe	Asn	Asn	Tyr	Asn	Val	Asn	Gln	Pro	Arg	His	Phe	Cys	Lys	His	Cys	
				85					90					95		
Gln	Arg	Tyr	Trp	Thr	Ala	Gly	Gly	Ala	Met	Arg	Asn	Val	Pro	Val	Gly	

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Ala	Gly	Arg	100	Arg	Lys	Asn	Lys	Asn	105	Ala	Thr	Ala	Ala	Ala	110	His	Phe	Leu
His	Arg	115	Arg	Ala	Cys	Ala	Ala	Ala	120	Ala	Ala	Ala	Met	Pro	125	Ala	Ala	Pro
His	Asp	130	Ala	Thr	Asn	135	Ala	Thr	Val	Leu	Ser	Phe	Gly	Gly	Gly	Gly	Gly	140
Gly	His	145	Asp	Ala	Leu	150	Pro	Val	Thr	Leu	Asp	155	Leu	Ala	Asp	Lys	Met	160
Arg	Leu	Gly	165	Lys	Glu	Gly	Leu	Val	Ala	His	170	Ala	Arg	Asn	175	Ala	Asp	Ala
Ala	Ala	Ala	180	Cys	Ser	Glu	Val	Ser	185	Ser	Asn	Arg	Asp	Asp	190	Glu	Gln	Ile
Gly	Asn	195	Thr	Val	Ala	Lys	Pro	Ala	200	Asn	Gly	Leu	Gln	Gln	205	His	Pro	Pro
Pro	Pro	210	His	His	His	His	His	Ser	215	Ala	Met	Asn	Gly	Gly	Gly	Ile	Trp	220
Pro	225	Tyr	Tyr	Thr	Ser	230	Gly	Ile	Ala	Ile	Pro	235	Ile	Tyr	Pro	Ala	Ala	Pro
Ala	Tyr	Trp	Gly	245	Cys	Met	Ile	Pro	Pro	250	Gly	Ala	Trp	Ser	255	Leu	Pro	260
Trp	Pro	Ala	Thr	Val	Gln	Ser	Gln	Ala	265	Ile	Ser	Ser	Ser	Ser	270	Pro	Pro	275
Thr	Ser	280	Ala	Thr	Pro	Ser	Val	Ser	285	Ser	Phe	Thr	Leu	Gly	Lys	His	Pro	290
Arg	Glu	Gly	Gly	Asp	His	300	Glu	Ala	Arg	Asp	His	305	His	Gly	Asn	Gly	Lys	310
Val	Trp	Val	Pro	Lys	Thr	Ile	Arg	Ile	Asp	315	Asn	Ala	Asp	Glu	Val	Ala	320	325
Arg	Ser	Ser	Ile	Arg	Ser	Leu	Phe	Ala	330	Phe	Arg	Gly	Gly	Asp	Lys	Val	335	340
Asp	Asp	Asn	345	Asp	Asp	Asp	Gly	Thr	Ser	Val	His	Lys	Leu	Ala	Thr	350	355	360
Thr	Val	Phe	Glu	Pro	Lys	Arg	Asp	Gly	Lys	Thr	Ala	Lys	His	Pro	Ala	365	370	375
Ile	Thr	Ser	Leu	Pro	Leu	Leu	His	Thr	Asn	Pro	380	Val	Ala	Leu	Thr	Arg	385	390
Ser	Ala	Thr	Phe	Gln	Glu	Gly	Ser		395								400	405

<210> 61
 <211> 290
 <212> PRT
 <213> Oryza sativa

<220>
 <221> PEPTIDE
 <222> (0)...(0)
 <223> line 1C-041-47 polypeptide sequence

<400> 61
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 1 5 10 15
 Ala Met Lys Glu Gln Lys Phe Glu Ser Tyr Phe Gly Arg Arg Ile Ala
 20 25 30
 Val Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ser Phe Ala Arg Tyr
 35 40 45
 Ser Lys Arg Glu Asp Ala Thr Lys Glu Leu Thr Glu Ala Val Glu Glu
 50 55 60
 Gly Asp Lys Asp Ala Ile Glu Lys Phe Ser Lys Arg Thr Val Lys Val
 65 70 75 80
 Thr Lys Gln His Asn Glu Glu Cys Lys Arg Leu Leu Arg Leu Met Gly

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[illegible]

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<210> 62
<211> 552
<212> PRT
<213> Oryza sativa
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<220>  
<221> PEPTIDE  
<222> (0)...(0)  
<223> line 1C-064-20 polypeptide sequence
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Pro	Ala	Val	Gly	Ile	Asp	Leu	Gly	Thr	Thr	Tyr	Ser	Cys	Val	Ala	Val
			20					25					30		
Trp	Arg	His	Asp	Arg	Gly	Glu	Val	Ile	Ala	Asn	Asp	Gln	Arg	Asn	Arg
		35					40					45			
Leu	Thr	Pro	Ser	Cys	Val	Ala	Phe	Thr	Ala	Asp	Asp	Asp	Asp	Ser	Phe
	50					55					60				
Val	Gly	Asp	Ala	Ala	Phe	Asn	Gln	Ser	Ala	Leu	Asn	Pro	Thr	Asn	Thr
65					70					75					80
Ile	Phe	Glu	Val	Lys	Arg	Leu	Ile	Gly	Arg	Arg	Phe	Ser	Asp	Asp	Ser
				85					90					95	
Val	Gln	Lys	Asp	Ile	Lys	Leu	Trp	Pro	Phe	Lys	Val	Val	Ala	Gly	Gln
			100					105					110		
Glu	Asp	Arg	Pro	Met	Ile	Val	Val	Arg	His	Glu	Gly	Glu	Glu	Arg	Gln
		115					120					125			
Phe	Met	Pro	Glu	Glu	Ile	Ser	Ser	Met	Val	Leu	Ala	Lys	Met	Arg	Glu
	130					135					140				
Thr	Ala	Glu	Val	Tyr	Leu	Gly	Lys	Thr	Val	Thr	Lys	Ala	Val	Ile	Thr
145					150					155					160
Val	Pro	Val	Tyr	Phe	Asn	Asn	Ala	Gln	Arg	Gln	Ala	Thr	Met	Asp	Ala
				165					170					175	
Gly	Ala	Ile	Ala	Gly	Leu	Asn	Val	Met	Arg	Ile	Ile	Asn	Glu	Pro	Thr

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Ala	Ala	Ala	180	Leu	Ala	Tyr	Cys	Leu	185	Glu	Lys	Met	Pro	Val	190	Ser	Asn	Lys
Gly	Arg	Met	195	Val	Leu	Val	Phe	Asp	200	Leu	Gly	Gly	Gly	Thr	205	Phe	Asp	Ile
Ser	Leu	Leu	210	Asn	Ile	Asp	215	Pro	Gly	Glu	Gly	Thr	220	Ala	Gly	Asp	Thr	His
225	Leu	Gly	Gly	Ala	Asp	230	Phe	Asp	Asn	Glu	Leu	Val	Lys	His	Ser	Leu	Arg	240
				245	Lys	His	Gly	Ser	Met	250	Asp	Ile	Glu	Ser	Asn	Gln	Lys	255
				260	Arg	Leu	Arg	Thr	Ala	265	Cys	Glu	Arg	Ala	Lys	Arg	Met	Leu
				275	Met	Gln	Thr	Thr	280	Ile	Glu	Val	Asp	Ser	Leu	His	Gln	Gly
				290	Thr	Met	Gln	Thr	295	Ile	Glu	Val	Asp	Ser	Leu	His	Gln	Gly
				305	Asp	Phe	Arg	Val	Thr	310	Leu	Thr	Arg	Ser	Arg	Phe	Glu	Glu
																		320
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<210> 63

<211> 479

<212> PRT

<213> Oryza sativa

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1C-109-35 polypeptide sequence

<400> 63

Met Ser Ser Ser Ala Thr Val Val Pro Leu Ala Tyr Gln Gly Asn Thr

1 5 10 15

Ser Ala Ser Val Ala Asp Trp Leu Asn Lys Gly Asp Asn Ala Trp Gln

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20 25 30
 Leu Val Ala Thr Leu Val Gly Leu Gln Ser Val Pro Gly Leu Val
 35 40 45
 Val Leu Tyr Gly Gly Val Val Lys Lys Lys Trp Ala Val Asn Ser Ala
 50 55 60
 Phe Met Ala Leu Tyr Ala Phe Ala Ala Val Trp Ile Cys Trp Val Thr
 65 70 75 80
 Trp Ala Tyr Asn Met Ser Phe Gly Glu Lys Leu Leu Pro Ile Trp Gly
 85 90 95
 Lys Ala Arg Pro Ala Leu Asp Gln Gly Leu Leu Val Gly Arg Ala Ala
 100 105 110
 Leu Pro Ala Thr Val His Tyr Arg Ala Asp Gly Ser Val Glu Thr Ala
 115 120 125
 Ala Val Glu Pro Leu Tyr Pro Met Ala Thr Val Val Tyr Phe Gln Cys
 130 135 140
 Val Phe Ala Ala Ile Thr Leu Ile Leu Val Ala Gly Ser Leu Leu Gly
 145 150 155 160
 Arg Met Ser Phe Leu Ala Trp Met Ile Phe Val Pro Leu Trp Leu Thr
 165 170 175
 Phe Ser Tyr Thr Val Gly Ala Phe Ser Leu Trp Gly Gly Gly Phe Leu
 180 185 190
 Phe His Trp Gly Val Ile Asp Tyr Cys Gly Gly Tyr Val Ile His Val
 195 200 205
 Ser Ala Gly Ile Ala Gly Phe Thr Ala Ala Tyr Trp Val Gly Pro Arg
 210 215 220
 Ala Gln Lys Asp Arg Glu Arg Phe Pro Pro Asn Asn Ile Leu Phe Thr
 225 230 235 240
 Leu Thr Gly Ala Gly Leu Leu Trp Met Gly Trp Ala Gly Phe Asn Gly
 245 250 255
 Gly Gly Pro Tyr Ala Ala Asn Ser Val Ala Ser Met Ala Val Leu Asn
 260 265 270
 Thr Asn Ile Cys Thr Ala Met Ser Leu Ile Val Trp Thr Cys Leu Asp
 275 280 285
 Val Ile Phe Phe Lys Lys Pro Ser Val Val Gly Ala Val Gln Gly Met
 290 295 300
 Ile Thr Gly Leu Val Cys Ile Thr Pro Ala Ala Gly Val Val Gln Gly
 305 310 315 320
 Trp Ala Ala Leu Val Met Gly Val Leu Ala Gly Ser Ile Pro Trp Tyr
 325 330 335
 Thr Met Met Ile Leu His Lys Arg Ser Lys Ile Leu Gln Arg Val Asp
 340 345 350
 Asp Thr Leu Gly Val Phe His Thr His Gly Val Ala Gly Leu Leu Gly
 355 360 365
 Gly Leu Leu Thr Gly Leu Phe Ala Glu Pro Thr Leu Cys Asn Leu Phe
 370 375 380
 Leu Pro Val Ala Asp Ser Arg Gly Ala Phe Tyr Gly Gly Ala Gly Gly
 385 390 395 400
 Ala Gln Phe Gly Lys Gln Ile Ala Gly Gly Leu Phe Val Val Ala Trp
 405 410 415
 Asn Val Val Val Thr Ser Leu Ile Cys Leu Ala Ile Asn Leu Leu Val
 420 425 430
 Pro Leu Arg Met Pro Asp Asp Lys Leu Glu Val Gly Asp Asp Ala Val
 435 440 445
 His Gly Glu Glu Ala Tyr Ala Leu Trp Gly Asp Gly Glu Met Tyr Asp
 450 455 460
 Val Thr Lys His Gly Ser Asp Ala Ala Val Ala Pro Val Val Val
 465 470 475

<210> 64
 <211> 2177
 <212> PRT
 <213> Oryza sativa

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1C-109-51 polypeptide sequence

<400> 64

Met	Ala	Asn	Leu	Gly	Gly	Gly	Ala	Glu	Ala	His	Ala	Arg	Phe	Lys	Gln
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Tyr	Glu	Tyr	Arg	Ala	Asn	Ser	Ser	Leu	Val	Leu	Thr	Thr	Asp	Ser	Arg
			20					25					30		
Pro	Arg	Asp	Thr	His	Glu	Pro	Thr	Gly	Glu	Pro	Glu	Thr	Leu	Trp	Gly
		35					40					45			
Arg	Ile	Asp	Pro	Arg	Ser	Phe	Gly	Asp	Arg	Ala	Val	Gln	Ala	Lys	Pro
	50					55					60				
Pro	Glu	Leu	Glu	Glu	Lys	Leu	Thr	Lys	Ser	Arg	Lys	Lys	Lys	Ala	Ala
65					70					75					80
Ala	Ser	Asp	Pro	Asp	Asp	Leu	His	Arg	Arg	Asp	Ala	Lys	Arg	Arg	Arg
				85					90					95	
Arg	Ala	Ala	Ala	Ala	Gln	Ser	Glu	Val	Ser	Val	Leu	Ser	Leu	Thr	Asp
			100					105					110		
Asp	Val	Val	Tyr	Lys	Pro	Gln	Thr	Lys	Glu	Thr	Arg	Ala	Ala	Tyr	Glu
	115						120					125			
Ala	Leu	Leu	Ser	Val	Ile	Gln	Gln	Gln	Phe	Gly	Gly	Gln	Pro	Leu	Asp
	130					135					140				
Val	Leu	Gly	Gly	Ala	Ala	Asp	Glu	Val	Leu	Ala	Val	Leu	Lys	Asn	Asp
145					150					155					160
Lys	Ile	Lys	Ser	Pro	Asp	Lys	Lys	Lys	Glu	Ile	Glu	Lys	Leu	Leu	Asn
				165					170					175	
Pro	Ile	Ser	Asn	Gln	Met	Phe	Asp	Gln	Ile	Val	Ser	Ile	Gly	Lys	Leu
			180					185					190		
Ile	Thr	Asp	Phe	His	Asp	Ala	Ser	Ala	Gly	Asp	Ser	Ala	Ala	Ala	Pro
		195					200					205			
Ser	Gly	Asp	Gly	Met	Asp	Thr	Ala	Leu	Asp	Asp	Asp	Ile	Gly	Val	Ala
	210					215					220				
Val	Glu	Phe	Glu	Glu	Asn	Glu	Asp	Asp	Glu	Glu	Ser	Asp	Phe	Asp	Gln
	225				230					235					240
Val	Gln	Asp	Asp	Leu	Asp	Glu	Asp	Glu	Asp	Asp	Asp	Leu	Pro	Glu	Ser
				245					250					255	
Asn	Ala	Pro	Gly	Ala	Met	Gln	Met	Gly	Gly	Glu	Leu	Asp	Asp	Asp	Asp
			260					265					270		
Met	Gln	Asn	Ser	Asn	Glu	Gly	Leu	Thr	Ile	Asn	Val	Gln	Asp	Ile	Asp
		275					280					285			
Ala	Tyr	Trp	Leu	Gln	Arg	Lys	Val	Ser	Gln	Ala	Tyr	Glu	Asp	Ile	Asp
	290					295					300				
Pro	Gln	His	Ser	Gln	Lys	Leu	Ala	Glu	Glu	Ile	Leu	Lys	Ile	Ile	Ala
	305				310					315					320
Glu	Gly	Asp	Asp	Arg	Asp	Val	Glu	Asn	Arg	Leu	Val	Met	Leu	Leu	Asp
				325					330				335		
Tyr	Glu	Lys	Phe	Asp	Leu	Ile	Lys	Leu	Leu	Leu	Arg	Asn	Arg	Leu	Lys
			340					345					350		
Ile	Val	Trp	Cys	Thr	Arg	Leu	Ala	Arg	Ala	Glu	Asp	Gln	Glu	Gln	Arg
		355					360					365			
Lys	Lys	Ile	Glu	Glu	Asp	Met	Gly	Asn	Pro	Thr	Leu	Thr	Pro	Ile	
	370					375				380					
Leu	Glu	Gln	Leu	His	Ala	Thr	Arg	Ala	Ser	Ala	Lys	Glu	Arg	Gln	Lys
	385				390					395					400
Asn	Leu	Glu	Lys	Ser	Ile	Arg	Asp	Glu	Ala	Lys	Arg	Leu	Thr	Lys	Ser
				405					410					415	
Glu	Asn	Thr	Gly	Ile	Asp	Gly	Ala	Arg	Asp	Arg	Arg	Ala	Val	Asp	Arg
			420					425					430		
Asp	Met	Glu	Ser	Gly	Trp	Leu	Lys	Gly	Gln	Arg	Gln	Leu	Leu	Asp	Leu
		435					440					445			

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Asp	Ser	Leu	Ser	Phe	His	Gln	Gly	Gly	Leu	Leu	Met	Ala	Asn	Lys	Lys
450						455					460				
Cys	Glu	Leu	Pro	Pro	Gly	Ser	Phe	Arg	Thr	Pro	His	Lys	Gly	Tyr	Glu
465					470					475					480
Glu	Val	His	Val	Pro	Ala	Leu	Lys	Ala	Lys	Pro	Tyr	Glu	Thr	Gly	Glu
				485					490					495	
Lys	Ile	Val	Lys	Ile	Ser	Asp	Met	Pro	Glu	Trp	Ala	Gln	Pro	Ala	Phe
			500					505					510		
Ala	Lys	Met	Thr	Gln	Leu	Asn	Arg	Val	Gln	Ser	Lys	Val	Tyr	Glu	Thr
		515					520					525			
Ala	Leu	Phe	Lys	Pro	Asp	Asn	Ile	Leu	Leu	Cys	Ala	Pro	Thr	Gly	Ala
		530				535					540				
Gly	Lys	Thr	Asn	Val	Ala	Val	Leu	Thr	Ile	Leu	Gln	Gln	Ile	Gly	Leu
545					550					555					560
His	Met	Lys	Asp	Gly	Val	Phe	Asp	Asn	Thr	Lys	Tyr	Lys	Ile	Val	Tyr
				565					570					575	
Val	Ala	Pro	Met	Lys	Ala	Leu	Val	Ala	Glu	Val	Val	Gly	Asn	Leu	Ser
			580					585					590		
Ala	Arg	Leu	Ser	Ala	Tyr	Gly	Ile	Thr	Val	Arg	Glu	Leu	Ser	Gly	Asp
		595					600					605			
Gln	Asn	Leu	Thr	Lys	Gln	Gln	Ile	Asp	Glu	Thr	Gln	Ile	Ile	Val	Thr
	610				615						620				
Thr	Pro	Glu	Lys	Trp	Asp	Ile	Val	Thr	Arg	Lys	Ser	Gly	Asp	Arg	Thr
625					630					635					640
Tyr	Thr	Gln	Met	Val	Lys	Leu	Leu	Ile	Ile	Asp	Glu	Ile	His	Leu	Leu
				645					650					655	
His	Asp	Asn	Arg	Gly	Pro	Val	Leu	Glu	Ser	Ile	Val	Ser	Arg	Thr	Val
		660						665					670		
Arg	Gln	Ile	Glu	Thr	Thr	Lys	Glu	His	Ile	Arg	Leu	Val	Gly	Leu	Ser
		675					680					685			
Ala	Thr	Leu	Pro	Asn	Tyr	Glu	Asp	Val	Ala	Val	Phe	Leu	Arg	Val	Arg
		690				695					700				
Ser	Asp	Gly	Leu	Phe	His	Phe	Asp	Asn	Ser	Tyr	Arg	Pro	Cys	Pro	Leu
705					710					715					720
Ala	Gln	Gln	Tyr	Ile	Gly	Ile	Thr	Val	Arg	Lys	Pro	Leu	Gln	Arg	Phe
				725					730					735	
Gln	Leu	Met	Asn	Glu	Ile	Cys	Tyr	Glu	Lys	Val	Met	Ala	Ser	Ala	Gly
			740					745					750		
Lys	His	Gln	Val	Leu	Ile	Phe	Val	His	Ser	Arg	Lys	Glu	Thr	Ala	Lys
		755					760					765			
Thr	Ala	Arg	Ala	Ile	Arg	Asp	Thr	Ala	Leu	Ala	Asn	Asp	Thr	Leu	Asn
		770				775					780				
Arg	Phe	Leu	Lys	Asp	Asp	Ser	Ala	Ser	Gln	Glu	Ile	Leu	Gly	Ser	Gln
785					790					795					800
Ala	Glu	Leu	Val	Lys	Ser	Ser	Asp	Leu	Lys	Asp	Leu	Leu	Pro	Tyr	Gly
				805					810					815	
Phe	Ala	Ile	His	His	Ala	Gly	Leu	Ala	Arg	Val	Asp	Arg	Glu	Leu	Val
			820					825					830		
Glu	Glu	Leu	Phe	Ala	Asp	Lys	His	Ile	Gln	Val	Leu	Val	Ser	Thr	Ala
		835					840					845			
Thr	Leu	Ala	Trp	Gly	Val	Asn	Leu	Pro	Ala	His	Thr	Val	Ile	Ile	Lys
		850				855					860				
Gly	Thr	Gln	Ile	Tyr	Asn	Pro	Glu	Lys	Gly	Ala	Trp	Thr	Glu	Leu	Ser
865					870					875					880
Pro	Leu	Asp	Val	Met	Gln	Met	Leu	Gly	Arg	Ala	Gly	Arg	Pro	Gln	Tyr
				885					890					895	
Asp	Thr	His	Gly	Glu	Gly	Ile	Ile	Leu	Thr	Gly	His	Ser	Glu	Leu	Gln
			900					905					910		
Tyr	Tyr	Leu	Ser	Leu	Met	Asn	Gln	Leu	Pro	Ile	Glu	Ser	Gln	Phe	
			915				920				925				
Ile	Ser	Arg	Leu	Ala	Asp	Gln	Leu	Asn	Ala	Glu	Ile	Val	Leu	Gly	Thr
			930			935					940				
Ile	Gln	Asn	Ala	Arg	Glu	Ala	Cys	Ser	Trp	Leu	Gly	Tyr	Thr	Tyr	Leu

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945 Tyr Ile Arg Met Leu 950 Arg Asn Pro Thr Leu 955 Tyr Gly Leu Pro Ala 960 Asp
 Ile Met Glu Thr 965 Asp Lys Thr Leu Asp 970 Glu Arg Arg Ala Asp 975 Leu Val
 His Ser Ala Ala Asn Leu Leu Asp 985 Arg Asn Asn Leu Ile 990 Lys Tyr Asp
 Arg Lys Thr Gly Tyr Phe 1000 Val Thr Asp Leu Gly Arg Ile Ala Ser
 Tyr Tyr Tyr Ile Ser His Gly Thr Ile Ser Thr Tyr Asn Glu Tyr Leu
 1025 Lys Pro Thr Met Gly Asp Ile Glu Leu Cys Arg Leu Phe Ser Leu Ser
 Glu Glu Phe Lys Tyr Val Ser Val Arg Gln Asp Glu Lys Met Glu Leu
 Ala Lys Leu Leu Asp Arg Val Pro Ile Pro Val Lys Glu Ser Leu Glu
 Glu Pro Ser Ala Lys Ile Asn Val Leu Leu Gln Ala Tyr Ile Ser Arg
 Leu Lys Leu Glu Gly Leu Ser Leu Ser Ser Asp Met Val Tyr Ile Arg
 1105 Gln Ser Ala Gly Arg Leu Leu Arg Ala Leu Phe Glu Ile Val Leu Lys
 Arg Gly Trp Ala Gln Leu Ala Glu Lys Ala Leu Asn Leu Cys Lys Met
 Ile Asp Lys Gln Met Trp Asn Val Gln Thr Pro Leu Arg Gln Phe Pro
 Gly Ile Pro Lys Glu Ile Leu Met Lys Leu Glu Lys Lys Glu Leu Ala
 Trp Glu Arg Tyr Tyr Asp Leu Ser Ser Gln Glu Ile Gly Glu Leu Ile
 1185 Arg Phe Pro Lys Met Gly Arg Gln Leu His Lys Cys Ile His Gln Leu
 Pro Lys Leu Asn Leu Ser Ala His Val Gln Pro Ile Thr Arg Thr Val
 Leu Gly Phe Glu Leu Thr Ile Thr Pro Asp Phe Gln Trp Asp Asp Lys
 Val His Gly Tyr Val Glu Pro Phe Trp Val Ile Val Glu Asp Asn Asp
 Gly Glu Asn Ile Leu His His Glu Tyr Phe Met Val Lys Lys Gln Tyr
 1265 Val Asp Glu Asp His Thr Leu Asn Phe Thr Val Pro Ile Tyr Glu Pro
 Leu Pro Pro Gln Tyr Phe Ile Arg Val Val Ser Asp Lys Trp Leu Gly
 Ser Gln Thr Ile Leu Pro Val Cys Phe Arg His Leu Ile Leu Pro Glu
 Lys Tyr Ala Pro Pro Thr Glu Leu Leu Asp Leu Gln Pro Leu Pro Val
 Thr Ala Leu Arg Asn Ala Arg Tyr Glu Gly Leu Tyr Ser Ala Phe Lys
 1345 His Phe Asn Pro Ile Gln Thr Gln Val Phe Thr Val Leu Tyr Asn Thr
 Asp Asp Ser Val Leu Val Ala Ala Pro Thr Gly Ser Gly Lys Thr Ile
 Cys Ala Glu Phe Ala Ile Leu Arg Asn His Gln Lys Ala Val Ser Gly
 Glu Ser Asn Met Arg Val Val Tyr Ile Ala Pro Ile Glu Ala Leu Ala
 1410 Lys Glu Arg Tyr Arg Asp Trp Glu Gln Lys Phe Gly Glu Phe Ala Arg
 1425 Val Val Glu Leu Thr Gly Glu Thr Ala Ala Asp Leu Lys Leu Leu Asp
 1445 1450 1455

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Lys Gly Glu Ile Ile Ile Ser Thr Pro Glu Lys Trp Asp Ala Leu Ser
 1460 1465 1470
 Arg Arg Trp Lys Gln Arg Lys Gln Val Gln Gln Val Ser Leu Phe Ile
 1475 1480 1485
 Val Asp Glu Leu His Leu Ile Gly Ser Glu Lys Gly His Val Leu Glu
 1490 1495 1500
 Val Ile Val Ser Arg Met Arg Arg Ile Ala Ser His Ile Gly Ser Asn
 1505 1510 1515 1520
 Ile Arg Ile Val Ala Leu Ser Ala Ser Leu Ala Asn Ala Lys Asp Leu
 1525 1530 1535
 Gly Glu Trp Ile Gly Ala Thr Ser His Gly Leu Phe Asn Phe Pro Pro
 1540 1545 1550
 Ala Val Arg Pro Val Pro Leu Glu Ile His Ile Gln Gly Val Asp Ile
 1555 1560 1565
 Ala Asn Phe Glu Ala Arg Met Gln Ala Met Thr Lys Pro Thr Tyr Thr
 1570 1575 1580
 Ala Ile Thr Gln His Ala Lys Asn Gly Lys Pro Ala Leu Val Phe Val
 1585 1590 1595 1600
 Pro Thr Arg Lys His Ala Arg Leu Thr Ala Leu Asp Leu Cys Ala Tyr
 1605 1610 1615
 Ser Ser Ala Glu Gly Gly Gly Thr Pro Phe Leu Leu Gly Ser Glu Asp
 1620 1625 1630
 Glu Met Asp Ala Phe Thr Gly Gly Ile Ser Asp Glu Thr Leu Lys Tyr
 1635 1640 1645
 Thr Leu Lys Cys Gly Val Gly Tyr Leu His Glu Gly Leu Ser Asp Leu
 1650 1655 1660
 Glu Gln Glu Val Val Thr Gln Leu Phe Leu Ser Gly Arg Ile Gln Val
 1665 1670 1675 1680
 Cys Val Ala Ser Ser Thr Val Cys Trp Gly Arg Ser Leu Pro Ala His
 1685 1690 1695
 Leu Val Val Val Met Gly Thr Gln Tyr Asp Gly Arg Glu Asn Ala
 1700 1705 1710
 His Thr Asp Tyr Pro Ile Thr Asp Leu Leu Gln Met Met Gly His Ala
 1715 1720 1725
 Ser Arg Pro Leu Gln Asp Asn Ser Gly Lys Cys Val Ile Leu Cys His
 1730 1735 1740
 Ala Pro Arg Lys Glu Tyr Tyr Lys Lys Phe Leu Phe Glu Ala Phe Pro
 1745 1750 1755 1760
 Val Glu Ser His Leu His His Phe Leu His Asp His Met Asn Ala Glu
 1765 1770 1775
 Val Val Val Gly Val Ile Glu Asn Lys Gln Asp Ala Val Asp Tyr Leu
 1780 1785 1790
 Thr Trp Thr Phe Met Tyr Arg Arg Leu Thr Lys Asn Pro Asn Tyr Tyr
 1795 1800 1805
 Asn Leu Gln Gly Val Ser His Arg His Leu Ser Asp His Leu Ser Glu
 1810 1815 1820
 Leu Val Glu Thr Val Leu Asn Asp Leu Glu Ser Ser Lys Cys Val Ala
 1825 1830 1835 1840
 Ile Glu Glu Asp Met Tyr Leu Lys Pro Leu Asn Leu Gly Leu Ile Ala
 1845 1850 1855
 Ser Tyr Tyr Tyr Ile Ser Tyr Thr Thr Ile Glu Arg Phe Ser Ser Met
 1860 1865 1870
 Leu Thr Gln Lys Thr Lys Met Lys Gly Leu Leu Glu Ile Leu Ala Ser
 1875 1880 1885
 Ala Ser Glu Tyr Ala Glu Leu Pro Ser Arg Pro Gly Glu Glu Asp Phe
 1890 1895 1900
 Ile Glu Lys Leu Val Arg His Gln Arg Phe Ser Ile Glu Lys Pro Arg
 1905 1910 1915 1920
 Tyr Gly Asp Pro His Val Lys Ala Asn Ala Leu Leu Gln Ala His Phe
 1925 1930 1935
 Ser Arg His Thr Ile Leu Gly Asn Leu Ala Ala Asp Gln Arg Glu Ile
 1940 1945 1950
 Leu Leu Ser Ala His Arg Leu Leu Gln Ala Met Val Asp Val Ile Ser

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1955 1960 1965
 Ser Asn Gly Trp Leu Thr Leu Ala Leu Asn Ala Met Glu Leu Ser Gln
 1970 1975 1980
 Met Val Thr Gln Gly Met Trp Asp Arg Asp Ser Val Leu Leu Gln Leu
 1985 1990 1995 2000
 Pro His Phe Thr Lys Glu Leu Ala Arg Arg Cys Gln Glu Asn Glu Gly
 2005 2010 2015
 Arg Pro Ile Glu Ser Ile Phe Asp Leu Ala Glu Met Ser Ile Asp Glu
 2020 2025 2030
 Met Arg Asp Leu Leu Gln Gln Ser Asn Pro Gln Leu Gln Asp Ile Ile
 2035 2040 2045
 Glu Phe Phe Lys Arg Phe Pro Asn Val Asp Met Ala Tyr Glu Val Arg
 2050 2055 2060
 Glu Gly Asp Asp Ile Arg Ala Gly Asp Asn Val Thr Val Gln Val Thr
 2065 2070 2075 2080
 Leu Glu Arg Asp Met Thr Asn Leu Pro Ser Glu Val Gly Pro Val His
 2085 2090 2095
 Ala Pro Arg Tyr Pro Lys Pro Lys Glu Glu Trp Trp Leu Val Ile
 2100 2105 2110
 Gly Asp Ser Thr Asn Gln Leu Leu Ala Ile Lys Arg Val Ala Leu
 2115 2120 2125
 Gln Lys Arg Ala Arg Val Lys Leu Glu Phe Thr Ala Ala Ser Glu Ala
 2130 2135 2140
 Gly Arg Lys Glu Tyr Met Ile Tyr Leu Met Ser Asp Ser Tyr Leu Gly
 2145 2150 2155 2160
 Cys Asp Gln Glu Tyr Glu Phe Thr Val Asp Val Met Asp Ala Gly Gly
 2165 2170 2175
 Asp

<210> 65
 <211> 181
 <212> PRT
 <213> Oryza sativa

<220>
 <221> PEPTIDE
 <222> (0)...(0)
 <223> line 1C-056-07 polypeptide sequence

<400> 65
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 Leu Leu His Gly Tyr Lys Phe Asp Ser Ile Asn Thr Val Tyr Tyr Met
 20 25 30
 Ala Pro Phe Ala Thr Met Ile Leu Ala Leu Pro Ala Val Leu Leu Glu
 35 40 45
 Gly Gly Gly Val Val Thr Trp Phe Tyr Thr His Asp Ser Ile Ala Ser
 50 55 60
 Ala Leu Val Ile Ile Ile Gly Ser Gly Val Leu Ala Phe Cys Leu Asn
 65 70 75 80
 Phe Ser Ile Phe Tyr Val Ile His Ser Thr Thr Ala Val Thr Phe Asn
 85 90 95
 Val Ala Gly Asn Leu Lys Val Ala Val Ala Val Leu Val Ser Trp Leu
 100 105 110
 Ile Phe Arg Asn Pro Ile Ser Pro Met Asn Ala Ile Gly Cys Ala Ile
 115 120 125
 Thr Leu Val Gly Cys Thr Phe Tyr Gly Tyr Val Arg His Leu Ile Ser
 130 135 140
 Gln Gln Gln Ala Val Ala Pro Gly Thr Gly Ser Pro Thr Thr Ser Gln
 145 150 155 160
 Thr Asn Ser Pro Arg Ser Arg Met Glu Met Leu Pro Leu Val Gly Asp

Lys Gln Glu Lys Val
180

<210> 66
<211> 793
<212> PRT
<213> Oryza sativa

<220>
<221> PEPTIDE
<222> (0)...(0)
<223> line 1C-100-32 polypeptide sequence

<400> 66
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Met Glu Ser Asp Val Ala Glu Glu Lys Arg Lys Arg Glu Asp Asp Ala
20 25 30
Ser Ser Ser Ala Val Leu Ala Ala Ala Asn Asn Thr Gly Gly Ala Gln
35 40 45
His Pro Met Trp Lys Thr Ser Leu Cys Ser Phe Phe Arg Arg Arg Ala
50 55 60
Ala Ser Ser Ala Asp Gly Cys Ser His Gly Asp Ser Cys Arg Tyr Ala
65 70 75 80
His ser Glu Glu Glu Leu Arg Pro Arg Pro Asp Gly Thr Trp Asp Pro
85 90 95
Thr Ser Asp Arg Ala Lys Lys Leu Arg Lys Val Ala Ala Asp Glu Val
100 105 110
Glu Glu Glu Val Val Thr Ile Asp Asp Lys Ala Leu Asp Lys Cys Leu
115 120 125
Val Gly Leu Pro Arg Gly Trp Ala Asn Asp Arg Leu Lys Thr Phe Leu
130 135 140
Gln Asp Lys Ala Arg Thr Asn Tyr Ser Ser Ile Leu Pro Pro Ala Leu
145 150 155 160
Leu Leu Gly Ile Ser Tyr Ala Thr Ala Lys Lys Lys Gly Met Thr
165 170 175
Val Gly Phe Val Thr Phe Glu Asn Ile Glu Gln Leu Lys Asn Ala Ile
180 185 190
Glu Val Leu Thr Glu Asn Gln Ser Gly Gly Lys Glu Ile Lys Ile Ala
195 200 205
Asp Ala Asn Arg Arg Ser His Gln Lys Leu His Thr Glu Lys Pro Val
210 215 220
Ser Asp Asn Gly Val Thr Thr Glu Asn Gly Thr Ser Val Asp Val Pro
225 230 235 240
Pro Gly Glu Thr Ser Ala Pro Glu Ala Ala Ile Ser Asn Lys Lys Ser
245 250 255
Val Arg Asp Ala Val Thr Pro Leu Ala His Met Ser Tyr Asn Asp Gln
260 265 270
Leu Glu His Lys Asn Asn Ser Val Ala Gln Ile Leu Lys Arg Leu Thr
275 280 285
Arg Asn Ala Arg Lys Ala Cys Pro Thr Gly Ile Pro Leu Pro Asp Trp
290 295 300
Val Phe Lys Ser Lys Glu Ile Gly Gly Leu Pro Cys Lys Leu Glu Gly
305 310 315 320
Ile Leu Glu Ser Pro Val Ile Asn Gly Tyr Arg Asn Lys Cys Glu Phe
325 330 335
Ser Val Gly Phe Ser Leu Glu Gly Lys Thr Val Gly Phe Met Leu
340 345 350
Gly Asn Phe Ser Thr Asp Met Ile Asp Lys Thr Lys Ser Arg Glu Gly
355 360 365
Val Thr Ala Val Glu Glu Pro Val Asp Cys Pro Asn Val Ser Glu Ile

	370					375					380					
Ser 385	Cys	Lys	Tyr	Ala	Leu 390	Met	Phe	Gln	Asp	Phe 395	Leu	Gln	Ser	Ser	Ser	400
Leu	Pro	Val	Trp	Asn 405	Arg	Val	Asn	Asn	Cys 410	Gly	Phe	Trp	Arg	Gln	Gln	415
Thr	Val	Arg	Glu 420	Gly	Arg	Cys	Arg	Ala 425	Gln	Ala	Val	Ala	Gln	Asn	Ala	430
Glu	Thr	Gln	Ile	Ser	Glu	Val	Met 440	Leu	Ile	Val	Gln	Val	Cys	Ser	Thr	445
Gly	Val 450	Asp	Asp	Ala	Val	Met 455	Lys	Asp	Glu	Phe	Asp 460	Lys	Leu	Thr	Val	465
Ala 465	Leu	Gln	Gln	Gly	Ala 470	Thr	Cys	Ser	Pro 475	Pro	Leu	Pro	Leu	Thr	480	485
Thr	Ile	Val	Val	Gln 485	Asp	His	Lys	Gly	Ile 490	Ser	Asn	Ala	Ala	Pro 495	Ala	500
Asp	Cys	Pro	Leu 500	Ile	Pro	Leu	Leu	Val 505	Pro	Lys	Val	Asp	Gln 510	Ser	Glu	515
Gly	Thr	Val 515	Asp	Lys	Thr	Arg	Ile 520	His	Asp	His	Ile	Gly 525	Asn	Leu	Trp	530
Phe	Ser 530	Ile	Ser	Pro	Thr	Ala 535	Phe	Phe	Gln	Val	Asn 540	Thr	Leu	Ala	Ala	545
Glu 545	Arg	Leu	Tyr	Thr	Leu 550	Ala	Gly	Asp	Trp	Ala 555	Asn	Leu	Asn	Ser	Gly 560	565
Thr	Leu	Leu	Phe	Asp 565	Val	Cys	Cys	Gly	Thr 570	Gly	Thr	Ile	Gly	Leu 575	Thr	580
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Ala	Val	Ser 595	Asp	Ala	Glu	Arg	Asn 600	Ala	Leu	Ile	Asn	Gly 605	Val	Ser	Asn	610
Cys	Arg 610	Phe	Val	Cys	Gly	Lys 615	Ala	Glu	Asp	Val	Met 620	Gly	Ser	Leu	Leu	625
Thr 625	Glu	Tyr	Leu	Gly	Ser 630	Pro	Gln	Gln	Asp	Ile 635	Pro	Val	Ser	Glu	Gly 640	645
Ala	Val	Ser	Gly	Thr 645	Val	Lys	Asp	Glu	Glu 650	Val	Ile	Asp	Ser	Ser 655	Lys	660
Asn	Ser	Gly	Glu 660	Asn	Leu	Asp	Ser	Ser 665	Met	Gln	Lys	Asn	Asp 670	Asn	Gly	675
Lys	Ser	Gln 675	Gln	Leu	Gly	Asp	Ala 680	Pro	Ala	Asp	Ser	Ser 685	Ser	Ser	Ala	690
Ile	Asp 690	Glu	Ile	Lys	Gly	Asn 695	Ser	Asn	Asp	Arg	Val 700	Gly	Asn	Gly	Leu	705
Glu 705	Gly	Ser	His	Asp	Glu 710	Tyr	Asn	Glu	Val	Ala 715	Gly	Glu	Asp	Ile	His 720	725
Gly	Glu	Ala	Ser	Leu 725	Ile	Asn	Glu	Ser	Val 730	Asp	Leu	Lys	Val	Ser 735	Asp	740
Cys	Leu	Glu	Asp 740	Arg	Lys	Thr	Ser	Asp 745	Gly	Ser	Ser	Ser 750	Ile	Ser	Asn	755
Asn	Asp	Val 755	Thr	Ala	Ala	Thr	Ala 760	Cys	Gln	Phe	Glu	Asp 765	Ile	Val	Ala	770
Ile	Val 770	Asp	Pro	Pro	Arg	Val 775	Gly	Leu	His	Pro	Thr 780	Val	Asn	Pro	Lys	785
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<210> 67
<211> 143
<212> PRT
<213> Oryza sativa
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<220>
<221> PEPTIDE
<222> (0)...(0)
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<223> line 1C-142-27 polypeptide sequence

<400> 67

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Phe Val Val Tyr Lys Ile Asp Glu Arg Ser Arg Ala Val Leu Val Asp
      35      40      45
Lys Val Gly Gly Pro Gly Glu Gly Tyr Glu Glu Leu Val Ala Ala Leu
      50      55      60
Pro Thr Asp Asp Cys Arg Tyr Ala Val Phe Asp Phe Asp Phe Val Thr
65      70      75      80
Val Asp Asn Cys Gln Lys Ser Lys Ile Phe Phe Ile Ala Trp Ser Pro
      85      90      95
Thr Ala Ser Arg Ile Arg Ala Lys Ile Leu Tyr Ala Thr Ser Lys Gln
      100      105      110
Gly Leu Arg Arg Val Leu Asp Gly Val His Tyr Glu Val Gln Ala Thr
      115      120      125
Asp Ser Ser Glu Met Gly Tyr Asp Val Ile Arg Gly Arg Ala Gln
      130      135      140

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<210> 68

<211> 452

<212> PRT

<213> Oryza sativa

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1C-140-04 polypeptide sequence

<400> 68

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Arg His Asp Phe Pro Glu Gly Phe Val Phe Gly Ala Gly Ser Ser Ala
      35      40      45
Phe Gln Val Glu Gly Ala Ala Ala Glu Asp Gly Arg Lys Pro Ser Ile
      50      55      60
Trp Asp Thr Phe Ile His Gln Gly Tyr Met Pro Asp Gly Ser Asn Ala
65      70      75      80
Asp Val Ser Ala Asp Gln Tyr His His Tyr Lys Glu Asp Val Lys Leu
      85      90      95
Met Tyr Asp Met Gly Leu Asp Ala Tyr Arg Phe Ser Ile Ala Trp Pro
      100      105      110
Arg Leu Ile Pro Asp Gly Arg Gly Glu Ile Asn Pro Lys Gly Leu Glu
      115      120      125
Tyr Tyr Asn Asn Leu Ile Asp Glu Leu Ile Met His Gly Ile Gln Pro
      130      135      140
His Val Thr Ile Tyr His Phe Asp Leu Pro Gln Ala Leu Gln Asp Glu
145      150      155      160
Tyr Gly Gly Ile Leu Ser Pro Arg Phe Ile Glu Asp Tyr Ser Ala Tyr
      165      170      175
Ala Glu Val Cys Phe Lys Asn Phe Gly Asp Arg Val Lys His Trp Ala
      180      185      190
Thr Phe Asn Gln Pro Asn Ile Glu Pro Ile Gly Gly Phe Asp Ala Gly
      195      200      205
Asp Arg Pro Pro Arg Arg Cys Ser Tyr Pro Phe Gly Thr Asn Cys Thr
210      215      220
Gly Gly Asp Ser Ser Thr Glu Pro Tyr Ile Val Ala His His Leu Leu

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225      230      235      240
Leu Ala His Ala Ser Ala Val Ser Ile Tyr Arg Gln Lys Tyr Gln Gln
      245      250      255
Ala Ile Gln Gly Gly Gln Ile Gly Ile Thr Leu Met Val Arg Trp His
      260      265      270
Glu Pro Tyr Thr Asp Lys Thr Ala Asp Ala Ala Ala Ile Arg Met
      275      280      285
Asn Glu Phe His Ile Gly Trp Phe Leu His Pro Leu Val His Gly Asp
      290      295      300
Tyr Pro Pro Val Met Arg Ser Arg Val Gly Gly Arg Leu Pro Ser Ile
      305      310      315      320
Thr Ala Ser Asp Ser Glu Lys Ile Arg Gly Ser Phe Asp Phe Ile Gly
      325      330      335
Ile Asn His Tyr Tyr Val Ile Phe Val Gln Ser Ile Asp Ala Asn Glu
      340      345      350
Gln Lys Leu Arg Asp Tyr Tyr Ile Asp Ala Gly Val Gln Gly Glu Asp
      355      360      365
Asp Lys Glu Asn Ile Gln Cys His Ser Trp Ser Leu Gly Lys Val Leu
      370      375      380
Asn His Leu Lys Leu Glu Tyr Gly Asn Pro Pro Val Met Ile His Glu
      385      390      395      400
Met Val Ile Gln Ile His Arg Ile Ser Ser Glu Arg Ser Thr Thr Thr
      405      410      415
Met Thr Ser Asp Arg Ser Ser Cys Arg Ala Thr Trp Lys Leu Cys Ile
      420      425      430
Cys Pro Tyr Gly Ala Leu Thr Leu Ala Thr Tyr Phe Leu Cys Ala
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Gly Lys Gly Ser
      450

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<210> 69
 <211> 6282
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> T-DNA sequence
 artificial sequence
 synthetic nucleic acid

<223> synthetic nucleic acid

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